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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C07K 14/705	A1	(11) International Publication Number: WO 99/21890 (43) International Publication Date: 6 May 1999 (06.05.99)
(21) International Application Number: PCT/SE98/01947 (22) International Filing Date: 27 October 1998 (27.10.98) (30) Priority Data: 9703914-3 27 October 1997 (27.10.97) SE 9800864-2 16 March 1998 (16.03.98) SE 9802575-2 17 July 1998 (17.07.98) SE (71) Applicant (for all designated States except US): ASTRA AKTIEBOLAG [SE/SE]; S-151 85 Södertälje (SE). (72) Inventor; and (75) Inventor/Applicant (for US only): EKSTRAND, Jonas [SE/SE]; Astra Hässle AB, Tvistevägen 48, S-907 36 Umeå (SE). (74) Agent: ASTRA AKTIEBOLAG; Patent Dept., S-151 85 Södertälje (SE).		(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>With international search report. Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>
(54) Title: NEW NUCLEOTIDE SEQUENCES		
(57) Abstract The present invention relates to a nucleic acid molecule encoding a GABA _B receptor, or a functionally equivalent modified form thereof, said receptor being selected from the group consisting of human and canine GABA _B receptors.		

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NEW NUCLEOTIDE SEQUENCES

TECHNICAL FIELD

- 5 The present invention relates in particular to nucleic acid molecules encoding GABA_B receptors, and to methods for screening for compounds which are inhibitors of transient lower esophageal sphincter relaxations (TLESR), said methods comprising the use of a nucleic acid molecule encoding a GABA_B receptor.

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BACKGROUND ART

GABA_B receptors

- 15 GABA (4-aminobutanoic acid) is an endogenous neurotransmitter in the central and peripheral nervous systems. Receptors for GABA have traditionally been divided into GABA_A and GABA_B receptor subtypes. GABA_B receptors (for a review see Kerr, D.I.B. and Ong, J. (1995) Pharmac. Ther. vol. 67, pp.187-246) belong to the superfamily of G-protein coupled receptors. GABA_B receptor agonists are described as being of use in the
- 20 treatment of CNS disorders, such as muscle relaxation in spinal spasticity, cardiovascular disorders, asthma, gut motility disorders such as irritable bowel syndrome and as prokinetic and anti-tussive agents. GABA_B receptor agonists have also been disclosed as useful in the treatment of emesis (WO 96/11680).
- 25 The cloning of the rat GABA_B receptors GABA_BR1a (SEQ ID NOS: 44 and 45) and GABA_BR1b (SEQ ID NOS: 46 and 47) is disclosed by Kaupmann et al. (1997) Nature, vol. 386, 239-246. The mature rat GABA_BR1b differed from GABA_BR1a in that the N-terminal 147 residues were replaced by 18 different residues. It was presumed that the rat GABA_BR1a and -b receptor variants are derived from the same gene by alternative
- 30 splicing.

The cloning of the human GABA_B receptor GABA_BR1b is disclosed in WO 97/46675.

Reflux

- 5 In some humans, the lower esophageal sphincter (LES) is prone to relaxing more frequently than in other humans. As a consequence, fluid from the stomach can pass into the esophagus since the mechanical barrier is temporarily lost at such times, an event hereinafter referred to as "reflux".
- 10 Gastro-esophageal reflux disease (GERD) is the most prevalent upper gastrointestinal tract disease. Current therapy has aimed at reducing gastric acid secretion, or by reducing esophageal acid exposure by enhancing esophageal clearance, lower esophageal sphincter tone and gastric emptying. The major mechanism behind reflux has been considered to depend on a hypotonic lower esophageal sphincter. However, recent research (e.g.
- 15 Holloway & Dent (1990) Gastroenterol. Clin. N. Amer. 19, 517-535) has shown that most reflux episodes occur during transient lower esophageal sphincter relaxations (TLESR), i.e. relaxations not triggered by swallows. It has also been shown that gastric acid secretion usually is normal in patients with GERD. Consequently, there is a need for compounds which reduce the incidence of TLESR and thereby prevent reflux.

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DISCLOSURE OF THE INVENTION

- In the applicants' earlier patent application WO 98/11885, filed on 15 September 1997, it is
- 25 disclosed that GABA_B receptor agonists can be used to reduce the incidence of transient lower esophageal sphincter relaxations (TLESR).

- The present invention provides nucleic acid molecules encoding human and canine GABA_B receptors. These nucleic acid molecules will make possible the screening for
- 30 compounds which are agonists or antagonists of GABA_B receptors, e.g. compounds which are inhibitors of transient lower esophageal sphincter relaxations (TLESR).

Consequently, in a first aspect, the present invention provides a nucleic acid molecule encoding a GABA_B receptor, or a functionally equivalent modified form thereof, said receptor being selected from the group consisting of human and canine GABA_B receptors.

5 In preferred forms of the invention, the said nucleic acid molecule encodes the human GABA_B receptor 1a (SEQ ID NOS: 48 and 49), 1b (SEQ ID NOS: 50 and 51), 1c (SEQ ID NOS: 54 and 55) or 1d (SEQ ID NOS: 56 and 57); or the canine GABA_B receptor 1a (SEQ ID NOS: 52 and 53) or 1c (SEQ ID NOS: 58 and 59). Accordingly, the invention furthermore provides a nucleic acid molecule selected from:

- 10 (a) nucleic acid molecules comprising a nucleotide sequence set forth as SEQ ID NO: 48, 50, 52, 54, 56 or 58;
- (b) nucleic acid molecules comprising a nucleotide sequence capable of hybridizing, under stringent hybridization conditions, to a nucleotide sequence complementary to the polypeptide coding region of a DNA molecule as defined in (a); and
- 15 (c) nucleic acid molecules comprising a nucleotide sequence which is degenerate as a result of the genetic code to a nucleotide sequence as defined in (a) or (b).

Furthermore, the invention provides nucleic acid molecules of genomic origin encoding human GABA_B receptors (SEQ ID NOS: 60 and 61) as well as nucleic acid molecules (set
20 forth as SEQ ID NO: 70, 72, 74, 76, 78, 80, 82, 84) encoding additional isoforms of the human GABA_B receptor which isoforms can be shown to be generated by alternative splicing.

It should thus be understood that the nucleic acid molecule according to the invention is
25 not to be limited strictly to molecules comprising the sequences set forth as SEQ ID : 48, 50, 52, 54, 56 or 58. Rather the invention encompasses nucleic acid molecules carrying modifications like substitutions, small deletions, insertions or inversions, which nevertheless encode proteins having substantially the biochemical activity of the GABA_B receptors according to the invention. Included in the invention are consequently nucleic
30 acid molecules, the nucleotide sequence of which is at least 95% homologous, preferably at least 96%, 97%, 98% or 99% homologous, with the nucleotide sequence shown as SEQ ID NO: 48, 50, 52, 54, 56 or 58 in the Sequence Listing.

The term "stringent hybridization conditions" is known in the art from standard protocols (e.g. Current Protocols in Molecular Biology, editors F. Ausubel et al., John Wiley and Sons, Inc. 1994) and could be understood as as stringent or more stringent than those
5 defined by e.g. hybridization to filter-bound DNA in 0.5 M NaHPO₄, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at +65°C, and washing in 0.1xSSC / 0.1% SDS at +68°C.

Included in the invention is also a nucleic acid molecule which nucleotide sequence is degenerate, because of the genetic code, to a nucleic acid of the present invention and more
10 particularly to one of the nucleotide sequences set forth as SEQ ID NOs: 48, 50, 52, 54, 56 and 58. A sequential grouping of three nucleotides, a "codon", codes for one amino acid. Since there are 64 possible codons, but only 20 natural amino acids, most amino acids are coded for by more than one codon. This natural "degeneracy", or "redundancy", of the genetic code is well known in the art. It will thus be appreciated that the nucleic acid
15 sequences shown in the Sequence Listing is only an example within a large but definite group of nucleic acid sequences which will encode the polypeptide as described above.

In a further aspect, the invention provides a recombinant polypeptide encoded by a nucleotide sequence of the present invention, encoding a GABA_B receptor. In preferred
20 forms of the inventions, the said polypeptide comprises an amino acid sequence set forth as SEQ ID NO: 49, 51, 53, 55, 57, 59, 71, 73, 75, 77, 79, 81, 83 or 85 in the Sequence Listing. However, polypeptides of the present invention are not to limited to those having an amino acid sequence identical with one of SEQ ID NOs: 49, 51, 53, 55, 59, 71, 73, 75, 77, 79, 81, 83 or 85 in the Sequence Listing. Rather the invention encompasses polypeptides carrying
25 modifications such as substitutions, small deletions, insertions or inversions, which polypeptides nevertheless have substantially the biological activities of the GABA_B receptor. Included in the invention are consequently polypeptides, the amino acid sequence of which is at least 95% homologous, preferably at least 96%, 97%, 98% or 99% homologous, with one of the amino acid sequences described by SEQ ID NOs: 49, 51, 53,
30 55, 57 59, 71, 73, 75, 77, 79, 81, 83 and 85 in the Sequence Listing.

Included in the invention are polypeptides of the present invention which have been post-translationally modified, e.g. by cleavage of an N-terminal signal sequence which can be e.g. 1 to 25 amino acids long.

- 5 In yet another aspect, the invention provides a vector transformed with a nucleic acid molecule of the present invention. The said vector can e.g. be a replicable expression vector which carries and is capable of mediating the expression of a nucleic acid molecule according to the invention. In the present context the term "replicable" means that the vector is able to replicate in a given type of host cell into which it has been introduced.
- 10 Examples of vectors are viruses such as bacteriophages, cosmids, plasmids and other recombination vectors. Nucleic acid molecules are inserted into vector genomes by methods well known in the art.

- 15 Included in the invention is also a cultured host cell harbouring a vector according to the invention. Such a host cell can be a prokaryotic cell, a unicellular eukaryotic cell or a cell derived from a multicellular organism. The host cell can thus e.g. be a bacterial cell such as an *E. coli* cell; a cell from a yeast such as *Saccharomyces cerevisiae* or *Pichia pastoris*, or a mammalian cell. The methods employed to effect introduction of the vector into the host cell are standard methods well-known to a person familiar with recombinant DNA
- 20 methods.

- A further aspect of the invention is a process for production of a GABA_B receptor polypeptide according to the invention, said process comprising culturing a host cell as defined above under conditions whereby the said polypeptide is produced, and recovering
- 25 the said polypeptide.

- A further important aspect of the invention is a method for the screening of compounds which are inhibitors of transient lower esophageal sphincter relaxations (TLESR), said method comprising the use of a nucleic acid molecule encoding a GABA_B receptor. The
- 30 said nucleic acid molecule encoding a GABA_B receptor can e.g. be one of the nucleic acid molecules according to the invention encoding human or canine GABA_B receptors.
- However, it should be understood that this aspect of the invention is not limited to the use

of the said human and canine GABA_B receptors, but rather encompasses the use of any GABA_B receptor for screening for compounds which are inhibitors of transient lower esophageal sphincter relaxations.

- 5 In yet another important aspect, the invention provides a method for the screening of compounds which are agonists or antagonists to a GABA_B receptor, said method comprising the use of a nucleic acid molecule, according to the invention, encoding human or canine GABA_B receptors.

10 Brief Description of the Drawings

Figure 1: Map of the human GABA_B receptor gene.

The exon/intron organisation is shown. Exons are indicated as solid boxes numbered 1-23.

- 15 The part of intron 5 that is retained together with exon 6 giving rise to GABA_B receptor 1b is indicated as an open box.

Figure 2: Expression of human GABA_B receptor 1b isoform in transfected C127 cells.

20

Western blot analysis of transfected C127 cells using a polyclonal anti-human GABA_B receptor antibody. Lane 1: Untransfected C127 whole cell lysate. Lanes 2-7: Whole cell lysates of six independent clones transfected with human GABA_B receptor 1b isoform encoding cDNA. The clones analysed in lanes 4 to 7 express a GABA_B receptor of

25 expected molecular weight (arrow).

Figure 3: Expression of human GABA_B receptor 1d isoform in transfected C127 cells.

- 30 Western blot analysis of transfected C127 cells using a polyclonal anti-human GABA_B receptor antibody. Lanes 1-3: Concentrated culture media from three independent C127 clones transfected with a cDNA expression construct encoding the human GABA_B receptor

1d isoform. Lanes 4-6: Whole cell lysates corresponding to the clones analysed in lanes 1-3. The experiment revealed that the human GABA_B receptor 1d cDNA encodes a secreted isoform. The arrow indicates the bands corresponding to the 1d isoform.

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Figure 4: Expression of human GABA_B receptor 1d isoform in *E. coli*.

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Western blot analysis of transformed *E. coli* cells using a polyclonal anti-human GABA_B receptor antibody. Lane 1: Lysate from an uninduced *E. coli* culture transformed with an pET-based expression construct encoding the human GABA_B receptor 1d cDNA. Lane 2: Lysate from an IPTG-induced *E. coli* culture transformed with an expression construct encoding the human GABA_B receptor 1d cDNA. Lane 3: Lysate from an IPTG-induced *E. coli* culture transformed with an expression construct encoding an unrelated protein. Lane 4: The BSA-conjugated peptide previously used for immunization was loaded on the gel as a positive antibody control.

15

The screening methods according to the invention can e.g. comprise the steps (a) transforming a cultured cell with a nucleic acid molecule encoding a GABA_B receptor, so that a GABA_B receptor is expressed on the surface of the cell; (b) contacting a test compound with the said cell; and (c) determining whether the test compound binds to, and/or activates, the GABA_B receptor.

20

In particular GABA_B receptor expressing cells, transgenic animals or cells and tissues derived thereof, may be used to screen substance libraries for antagonist or agonist activities. For this purpose, GABA_B receptor expression may be directed to cells and tissues containing, either naturally or artificially, the necessary components allowing correct receptor transport and processing as well as coupling to second messenger pathways. Screening may be performed as ligand binding assays or functional assays. For screening, cells and tissues may be prepared in various ways, each uniquely suited to its purpose. Ligand binding assays are performed *in vivo* or *in vitro* using e.g. radiolabelled GABA. Functional assays exemplified by, but not limited to, Ca⁺⁺-responses, cAMP-

30

responses and effects on K^+ channels, may be performed in living cells, broken cells, isolated cell membranes, as well as in tissues and in living animals. To facilitate measurement of physiological $GABA_B$ receptor mediated responses, $GABA_B$ receptors may be co-expressed with promiscuous G-proteins like e.g. $G\alpha 16$ or $Gq15$ increasing G-protein coupling. Another possible way to increase G-protein coupling is to fuse the $GABA_B$ receptor with appropriate G-proteins using standard molecular techniques. In order to further improve readouts in Ca^{++} -response assays, $GABA_B$ receptors may be co-expressed with aequorin, a photoprotein cloned from the luminescent jellyfish *Aequorea victoria*.

In yet another aspect, the invention provides a pharmaceutical compositions comprising a soluble $GABA_B$ receptor further comprising one or more pharmaceutical acceptable carriers and/or diluents.

In yet another aspect, the invention provides a method for the diagnosis or treatment of conditions related to GABA-dysfunction, e.g. epilepsy, psychiatric disorders such as depression and anxiety, cognitive dysfunction, gastroesophageal reflux disease, emesis, irritable bowel syndrome, dyspepsia, spasticity, arthritis, allergies, autoimmune diseases, neoplastic diseases, pain, and infectious diseases, comprising the use or administration of soluble forms of the $GABA_B$ receptor, such as the human $GABA_B$ receptor 1c or 1d or functionally equivalent modified forms thereof; preferably being a polypeptide of the present invention..

The soluble forms of the $GABA_B$ receptor can e.g. be produced by culturing a host cell harbouring a vector comprising a nucleic acid encoding the soluble $GABA_B$ receptor under conditions where whereby the said polypeptide is produced, the polypeptide recovered and administered to a patient in need thereof.

Furthermore, the level of soluble $GABA_B$ receptors in certain body fluids, e.g. serum and CSF, can be measured and used in diagnostics related to conditions with altered levels of soluble $GABA_B$ receptors in said body fluids.

Throughout this description the terms "standard protocols" and "standard procedures", when used in the context of molecular cloning techniques, are to be understood as protocols and procedures found in an ordinary laboratory manual such as: Current Protocols in Molecular Biology, editors F. Ausubel et al., John Wiley and Sons, Inc. 1994, or Sambrook, J., Fritsch, E.F. and Maniatis, T., Molecular Cloning: A laboratory manual, 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY 1989.

EXAMPLES

10

EXAMPLE 1A: Cloning and sequencing of cDNA encoding human GABA_B receptor 1a and 1b

15

Messenger RNA from human hippocampus was obtained from Clontech (Palo Alto, CA, USA) (catalog #6578-1). First-strand cDNA synthesis reactions were performed using the First-strand cDNA Synthesis kit from Amersham Pharmacia Biotech (Uppsala, Sweden). The pd(N)₆ primer was used to prime the first-strand synthesis. The generated cDNA molecules were used as template in the PCR reactions described below.

20

Specific PCR primers were designed (Table 1) based on the sequences of the rat GABA_B receptor 1a and 1b cDNA (Kaupmann et al. 1997, EMBL accession numbers Y10369 (SEQ ID NO: 44) and Y10370 (SEQ ID NO: 46)).

TABLE 1

Primers used for RT-PCR on mRNA from human hippocampus

Nr.	Species	Sequence 5' - 3'	SEQ ID NO
794	Rat	GTTTCTTCTCGGATCCAGCTGTGCCTG	1
795	Rat	CAGGCACAGCTGGATCCGAGAAGAAACT	2
796	Rat	CGGTCGACTCACTTGTAAGCAAATGTACTCGACTCCC	3
797	Rat	ATGCGCGCCGGCAGCCAACATGCTGCTGCTGCTGCTGGTGC	4
831	Rat	CGGTCGACTCACTTGTAAGCAAATGTACTCGACTCCCATCACAGC	5
838	Rat	ATGCGCGCCGGCAGCCAACATGCTGCTGCTGCTGCTGGTGCCTCTCTTCC	6
842	Rat	CAGGCACAGCTGGATCCGAGAAGAAACTCTGTCGGAAGT	7
863	Rat	GGTCATCCAGCGTTGAGGTGAAGAC	8
864	Rat	GAAGGTTGCCAGATTATACATCCGC	9
865	Rat	CCACGATGATTCGAGCATCTTGACG	10
866	Rat	GCCTCTCACTCCCCTCATCTCC	11
932	Human	GAGTGAAGGAGGCTGGAATTG	12

- 5 cDNA fragments encoding parts of the human GABA_B receptors were amplified directly by PCR using the designed primers with the generated cDNA molecules as templates. All PCR experiments were carried out using the Perkin Elmer Taq DNA polymerase with Gene Amp (Roche Molecular Systems Inc., NJ, USA) with the following PCR program: +95°C for 1 minute, +50°C for 30 seconds, +72°C for 3 minutes, repeated 44 times and finally
- 10 +72°C for 7 minutes. The following primer combinations gave PCR products with expected sizes: 838 and 842, 838 and 795, 797 and 865, 864 and 865, 864 and 863 which corresponds to the 5'-end of the GABA_B receptor 1a. Primer pair 932 and 831, 932 and 796, 794 and 831 gave PCR products which correspond to the 3'-end of both GABA_B receptor 1a and 1b. The primer combination 839 and 918 gave a PCR product
- 15 corresponding to the 5'-end of the GABA_B receptor 1b.

The PCR products were subcloned into the pGEM-T vector from Promega (Madison, USA). The inserts were subjected to nucleotide sequence analysis, the complete nucleotide sequence for all subclones were determined using a Thermo Sequenase dye terminator

20 cycle sequencing pre-mix kit (Amersham Pharmacia Biotech, Uppsala, Sweden). As primers for sequencing reactions specific oligonucleotides complementary to the vector pGEM-T or primers complementary to the cDNA encoding the GABA_B receptor were used.

Additional PCR primers were designed based on the obtained sequences encoding fragments of the human GABA_B receptor and additional DNA fragments encoding parts of the human GABA_B receptors were amplified by PCR, the PCR products subcloned and
5 sequenced as described above.

EXAMPLE 1B : Cloning and sequencing of the 3'-ends of the cDNA encoding human GABA_B receptors 1a and 1b

10

Messenger RNA from human hippocampus was obtained from Clontech (Palo Alto, CA, USA) (catalogue #6578-1). First strand cDNA synthesis reactions were performed using the First-strand cDNA Synthesis kit from Amersham Pharmacia Biotech (Uppsala, Sweden). The Not I-d(T)₁₈ primer was used to prime the first-strand synthesis. The
15 generated cDNA molecules were used as template in the PCR reactions described below.

Specific PCR primers were designed (Table 2) based on the sequences of the human GABA_B receptor 1a and 1b cDNA obtained in Example 1A and the EST sequence EMBL accession number Y11044.

20

By homology searches in the EMBL database using the GABA_B receptor cDNA sequences obtained in Example 1A as query the EST sequence EMBL accession number Y11044 have been found to be homologous to the 3'-end of the GABA_B receptor cDNA.

25 **TABLE 2**

Primers used in PCR to amplify 3'ends of human GABA_B receptor cDNA

Nr	Species	Sequence 5'-3'	SEQ ID NO
938	Human	GACGCTTATCGAGCAGCTTC	13
972	Human	AGCCCAGAACTCACAGGGGGACAT	14
973	Human	GCTTCAAGCCAGGTACGAACTAA	15

cDNA fragments encoding parts of the human GABA_B receptors were amplified directly by
30 PCR using the designed primers with the generated cDNA molecules as templates. All

PCR experiments were carried out using the Perkin Elmer Taq DNA polymerase with Gene Amp (Roche Molecular Systems Inc., NJ, USA) with the following PCR program: + 95°C for 1 minute, +50°C for 30 seconds, +72°C for 3 minutes, repeated 44 times and finally +72°C for 7 minutes. The following primer combinations gave PCR products with expected sizes: 938 and 972, 938 and 973 corresponding to the 3' end of both GABA_B receptor 1a and 1b cDNA.

The PCR products were subcloned into the pGEM-T vector from Promega (Madison, USA). The inserts were subjected to nucleotide sequence analysis, the complete nucleotide sequence for all subclones were determined using a Thermo Sequenase dye terminator cycle sequencing pre-mix kit (Amersham Pharmacia Biotech, Uppsala, Sweden). As primers for sequencing reactions specific oligonucleotides complementary to the vector pGEM-T or primers complementary to the cDNA encoding the GABA_B receptor were used.

EXAMPLE 1C : Cloning and sequencing of the 5'-end of the cDNA encoding human GABA_B receptor 1b

Messenger RNA from human hippocampus was obtained from Clontech (Palo Alto, CA, USA) (catalogue #6578-1). Marathon cDNA amplification Kit (Clontech) was used for performing 5'/3'- RACE (Rapid Amplification of cDNA Ends). Adaptor-ligated double stranded cDNA molecules were amplified according to the manufacturers description. The pd(N)₆ primer from the First-strand cDNA Synthesis kit from Amersham Pharmacia Biotech (Uppsala, Sweden) was used to produce the adaptor-ligated cDNA.

A specific PCR primer was designed (Table 3) based on the sequences of the human GABA_B receptor 1b cDNA obtained in Example 1A.

TABLE 3

Primers used in PCR to amplify the 5'-ends of human GABA_B receptor cDNA

Nr.	Species	Sequence 5'-3'	SEQ ID NO
958	Human	TGGCCCTCCACCGCCTCAGTCATCTCA	16
AP1	Marathon kit	CCATCCTAATACGACTCACTATAGGGC	17

- 5 cDNA fragments encoding part of the human GABA_B receptors were amplified directly by PCR using the designed primers with the generated adaptor-ligated cDNA molecules as template. The PCR experiment was carried out using the Expand Long Template PCR System (Boehringer Mannheim GmbH, Germany) with the following PCR program: + 94°C for 1 minute, + 94°C for 30 seconds, +60°C for 30 seconds, +68°C for 4 minutes, repeated 24 times. The primer combination AP1 and 958 gave a PCR product which corresponded to the 5'-end of the GABA_B receptor 1b cDNA, including 190 base pairs upstream the initiation codon.

- 15 The PCR products were subcloned into the pGEM-T vector from Promega (Madison, USA). The inserts were subjected to nucleotide sequence analysis, the complete nucleotide sequence for all subclones were determined using a Thermo Sequenase dye terminator cycle sequencing pre-mix kit (Amersham Pharmacia Biotech, Uppsala, Sweden). As primers for sequencing reactions specific oligonucleotides complementary to the vector pGEM-T or primers complementary to the cDNA encoding the GABA_B receptor were used.

EXAMPLE 1D : Cloning and sequencing of the 5'-end of the cDNA encoding human GABA_B receptor 1a

25

- Messenger RNA from human hippocampus was obtained from Clontech (Palo Alto, USA) (catalogue #6578-1). Marathon cDNA amplification Kit (Clontech) was used to obtain adaptor-ligated double stranded cDNA molecules according to the manufacturer's description. The pd(N)₆ primer from the First-strand cDNA Synthesis kit from Amersham Pharmacia Biotech (Uppsala, Sweden) was used to obtain the adaptor-ligated cDNA .

30

Specific PCR primers were designed (Table 4) based on the sequences of the human GABA_B receptor 1a cDNA obtained in Example 1 and the rat GABA_B receptor 1a cDNA disclosed in WO 97/46675.

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TABLE 4

Primers used to amplify 5'-ends of the human GABAB receptor 1a cDNA

Nr.	Species	Sequence 5'-3'	SEQ ID NO
1033	Human	CTCAATCTCATAGTCCACTGG	18
1087	Rat	CCTTGAGGCCCGGGGAGAG	19

10 cDNA fragments encoding part of the human GABAB 1a receptor were amplified directly by PCR using the designed primers with the generated adaptor-ligated cDNA molecules as template. The PCR was performed using the Perkin Elmer Taq DNA polymerase with Gene Amp (Roche Molecular Systems Inc., NJ, USA) with the following PCR program: +94°C for 1 minute, +50°C for 30 seconds, +72°C for 3 minutes; +94°C for 1 minute, +60°C
15 for 30 seconds, +72°C for 4 minutes, repeated 34 times and finally +72°C for 7 minutes.

The primer combination 1087 and 1033 gave a PCR product corresponding to the 5'-end of the GABA_B receptor 1a cDNA, including 26 base pairs upstream the initiation codon.

20 The PCR products were subcloned into the pGEM-T vector from Promega (Madison, USA). The inserts were subjected to nucleotide sequence analysis, the complete nucleotide sequence for all subclones were determined using a Thermo Sequenase dye terminator cycle sequencing pre-mix kit (Amersham Pharmacia Biotech, Uppsala, Sweden). As primers for sequencing reactions specific oligonucleotides complementary to the vector
25 pGEM-T were used.

A complete cDNA sequence encoding the human GABA_B receptors 1a (SEQ ID NO: 48) and the human GABA_B receptor 1b (SEQ ID NO: 50) were obtained by aligning the sequences of the different fragments cloned and sequenced in Examples 1A, 1B, 1C and
30 1D.

EXAMPLE 2A: Cloning and sequencing of cDNA encoding canine GABA_B receptor 1a

- 5 QuickPrep Micro mRNA Purification kit (Amersham Pharmacia Biotech, Uppsala, Sweden) was used to isolate mRNA from canine neural tissues according to the manufacturers description. First-strand cDNA synthesis reactions were performed using the First-strand cDNA Synthesis kit from Amersham Pharmacia Biotech (Uppsala, Sweden). The Not-I-d(T)₁₈ bifunctional or pd(N)₆ primer was used to prime the first-strand synthesis.
- 10 The generated cDNA molecules were used as template in the PCR reactions described below.

Specific PCR primers (Table 5) were designed based on the sequences of the rat GABA_B receptor 1a and 1b cDNA (Kaupmann et al. 1997, EMBL accession numbers Y10369 (SEQ ID NO: 44 and Y10370 (SEQ ID NO: 46)).

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TABLE 5

Primers used for RT-PCR on mRNA from canine cortex

Nr.	Species	Sequence 5'-3'	SEQ ID NO
795	Rat	CAGGCACAGCTGGATCCGAGAAGAACT	20
831	Rat	CGGTCGACTCACTTGTAAGCAAATGTACTCGACTCCCATCACAGC	21
838	Rat	ATGCGCGCCGGCAGCCAACATGCTGCTGCTGCTGCTGGTGCCTCTCTTCC	22
840	Rat	CGTCAAGATGCTCGAATCATCG	23
841	Rat	CAGGGGGCTCAGAGGGTCCC	24
842	Rat	CAGGCACAGCTGGATCCGAGAAGAACTCTGTGCGAAAGT	25
844	Rat	CGGTCGACTCACTTGTAAGCAAATGTACTCGACTCCCATCACAGCTAAG	26
848	Rat	ACTTTCGACAGAGTTTCTTCTCGGATCCAGCTGTGCCTG	27
865	Rat	CCACGATGATTCGAGCATCTTGACG	28

20

cDNA fragments encoding parts of the canine GABA_B receptor were amplified directly by PCR using the designed primers with the generated cDNA molecules as templates. All PCR experiments were carried out using the Perkin Elmer Taq DNA polymerase with Gene Amp (Roche Molecular Systems Inc., NJ, USA) with the following PCR program: +95°C for 1 minute, +50°C for 30 seconds, +72°C for 3 minutes, repeated 44 times and finally

25

+72°C for 7 minutes. The following primer combinations gave PCR products with expected sizes: 842 and 838, 838 and 795, 838 and 865 which corresponds to the 5'-part of the canine GABA_B receptor cDNA. Primer pair 848 and 844, 848 and 831, 848 and 841, 840 and 841 gave PCR products which correspond to the 3'-part of the canine GABA_B receptor cDNA.

The PCR products were subcloned into the pGEM-T vector from Promega (Madison, USA). The inserts were subjected to nucleotide sequence analysis, the complete nucleotide sequence for all subclones were determined using a Thermo Sequenase dye terminator cycle sequencing pre-mix kit (Amersham Pharmacia Biotech, Uppsala, Sweden). As primers for sequencing reactions specific oligonucleotides complementary to the vector pGEM-T or primers complementary to the cDNA encoding the GABA_B receptor were used.

EXAMPLE 2B: Cloning and sequencing of the 3'- and 5'-ends of the cDNA encoding canine GABA_B receptor 1a

QuickPrep Micro mRNA Purification kit (Amersham Pharmacia Biotech, Uppsala, Sweden) was used to isolate mRNA from canine nerve tissues according to the manufactures description. Marathon cDNA amplification Kit (Clontech, Palo Alto, CA, USA) were used for performing both 5'-and 3'-RACE. Two adaptor-ligated double stranded cDNA libraries were amplified according to the manufacturers description. A random primer (pd(N)₆) was used when amplifying the adaptor-ligated cDNA for the 5'-RACE and the Marathon cDNA Synthesis primer (52-mer) was used when amplifying the adaptor ligated cDNA for the 3'-RACE.

Specific PCR primers were designed (Table 6) based on the sequence of canine GABA_B receptor 1a cDNA obtained in Example 2A.

TABLE 6

Primers used in PCR to amplify the 5'- and 3'-ends of canine GABA_B receptor 1a cDNA

Nr.	Species	Sequence 5'-3'	SEQ ID NO
936	canine	CTACCGCGCAATGAACTCCTCGTC	29
1076	canine	CGAGGTGGCGTTGGGGGTCTGTGC	30
AP1	Marathon kit	CCATCCTAATACGACTCACTATAGGGC	31
AP2	Marathon kit	ACTCACTATAGGGCTCGAGCGGC	32

5 cDNA fragments encoding parts of the canine GABA_B receptor were amplified by PCR from the adaptor-ligated cDNA using the designed primers. A number of different PCR programs were tested to find conditions where PCR products corresponding to GABA_B receptor DNA were obtained. The 5'- PCR experiments were carried out using the Expand Long Template PCR System (Boehringer Mannheim GmbH, Germany) with the following
 10 PCR program: +94°C for 30 seconds, +72°C for 3 minutes, repeated 4 times; +94°C for 30 seconds, +70°C for 3 minutes, repeated 4 times; and +94°C for 30 seconds, +68°C for 3 minutes, repeated 24 times. The primer combination AP2 and 1076 gave a PCR product which corresponded to the 5'-end of the GABA_B receptor cDNA, including 114 base pairs upstream the initiation codon.

15

The 3'- PCR experiments were carried out using the Expand Long Template PCR System (Boehringer Mannheim GmbH, Germany) with the following PCR program: +94°C for 1 minute; and +94°C for 30 seconds, +60°C for 30 seconds, +68 °C for 4 minutes, repeated
 20 29 times. The primer combination AP1 and 936 gave a PCR fragment which corresponded to the 3'-end of the GABA_B receptor cDNA, including the poly(A) tail.

The PCR products were subcloned into the pGEM-T vector from Promega (Madison, USA). The inserts were subjected to nucleotide sequence analysis, the complete nucleotide sequence for all subclones were determined using a Thermo Sequenase dye terminator
 25 cycle sequencing pre-mix kit (Amersham Pharmacia Biotech, Uppsala, Sweden). As primers for sequencing reactions specific oligonucleotides complementary to the vector pGEM-T or primers complementary to GABA_B receptor DNA were used.

Complete cDNA sequence encoding the canine GABA_B receptor 1a (SEQ ID NO: 52) was obtained by aligning the sequences of the different fragments obtained in Example 2A and Example 2B.

5

EXAMPLE 3A: Cloning of cDNA encoding human GABA_B receptor 1c and 1d from Jurkat cells

A guanidinisothiocyanate/CsCl method was used to isolate total RNA from Jurkat cells.

10 The first-strand cDNA synthesis was performed using the First-strand cDNA Synthesis kit from Amersham Pharmacia Biotech (Uppsala, Sweden). The pd(N)₆ primer was used to prime the first strand synthesis. The generated cDNA molecules were used as templates in the PCR reaction described below.

15 Specific PCR primers (Table 7) were designed based on the sequence of human GABA_B receptor 1a and 1b cDNA (Example 1), rat GABA_B receptor (Kaupmann et al. 1997) and the EST sequence EMBL accession number Y11044.

TABLE 7

20 Primers used in RT-PCR on mRNA from Jurkat cells

Nr	Species	Sequence 5'-3'	SEQ ID NO
938	human	GACGCTTATCGAGCAGCTTC	33
972	human	AGCCCAGAACTCACAGGGGGACAT	34
973	human	GCTTCAAGCCAGGTACGAACTAA	35
893	rat	GGAGCACCCCCAAGCCCCACTG	36
937	human	CTGGTTCCTCCCAATGTG	37
1005	rat	CCTCTCACTCCCCTCATCTC	38
1030	human	AAGCCAACCTTCCCTGCTTCTC	39

cDNA fragments encoding parts of the GABA_B receptor were amplified directly by PCR using human and rat specific primers. All PCR experiments were carried out using the

25 Perkin Elmer Taq DNA polymerase with Gene Amp (Roche Molecular Systems Inc., NJ,

USA) with the following PCR program: +95°C for 1 minute; +54°C for 1 minutes, +72°C for 3 minutes, repeated 44 times; and finally +72°C for 7 minutes.

The PCR products were subcloned into the pGEM-T vector from Promega (Madison, USA). The inserts were subjected to nucleotide sequence analysis, the complete nucleotide sequence for all subclones were determined using a Thermo Sequenase dye terminator cycle sequencing pre-mix kit (Amersham Pharmacia Biotech, Uppsala, Sweden). As primers for sequencing reactions specific oligonucleotides complementary to the vector pGEM-T or primers complementary to GABA_B receptor DNA were used.

The following primer combination gave PCR products corresponding to the 3'-end of the GABA_B receptor cDNA: primer pairs 938 and 972; 938 and 973. Unexpectedly both these fragments lacked 149 base pairs, resulting in a frame shift and the insertion of a new termination codon. The following primer combination gave a PCR product corresponding to the 5'-part of the GABA_B receptor 1a cDNA: 893 and 937. The primer pairs 1005 and 937, 1030 and 937 gave PCR products corresponding to the 5'-part of the GABA_B receptor 1b cDNA. Also these PCR fragments lacked the same 149 base pairs which resulted in a frame shift and the insertion of a new termination codon.

These results show that Jurkat cells contain mRNA encoding two new forms of the human GABA_B receptor. These are designated GABA_B receptor 1c (SEQ ID NO: 54 and 55) (comprising the same 5'-part as the GABA_B receptor 1a) and GABA_B receptor 1d (SEQ ID NO: 56 and 57) (comprising the same 5'-part as the GABA_B receptor 1b). These two forms of the GABA_B receptor do not contain any of the transmembrane regions and are therefore expected to be soluble forms of the receptor.

EXAMPLE 3B: Analysis of cDNA encoding human GABA_B receptors from hippocampus

Messenger RNA from human hippocampus was obtained from Clontech (Palo Alto, USA) (catalogue #6578-1). First strand cDNA synthesis reactions were performed using the First-strand cDNA Synthesis kit from Amersham Pharmacia Biotech (Uppsala, Sweden). The

pd(N)₆ primer was used to prime the first-strand synthesis. The generated cDNA molecules were used as template in the PCR reactions described below.

Specific PCR primer was designed (Table 8) based on the sequences of the cDNAs encoding human GABA_B receptors 1a and 1b.

TABLE 8

Primers used for RT-PCR on mRNA from human hippocampus

Nr	Species	Sequence 5' - 3'	SEQ ID NO
937	Human	CTGGTTCCTCCCAATGTG	40
938	Human	GACGCTTATCGAGCAGCTTC	41

cDNA fragments encoding parts of the human GABA_B receptors were amplified directly by PCR using the designed primers with the generated cDNA molecules as templates. All PCR experiments were carried out using the Perkin Elmer Taq DNA polymerase with Gene Amp (Roche Molecular Systems Inc., NJ, USA) with the following PCR program: +94°C for 1 minute, +50°C for 30 seconds, +72°C for 3 minutes; +94°C for 1 minute, +54°C for 30 seconds, +72°C for 3 minutes repeated 44 times; and finally +72°C for 7 minutes. The primer combination 938 and 937 gave a PCR product which corresponded to the expected size of the GABA_B receptor 1a and 1b cDNA but also a fragment a smaller size.

The PCR products were subcloned into the pGEM-T vector from Promega (Madison, USA). The inserts were subjected to nucleotide sequence analysis, the complete nucleotide sequence for all subclones were determined using a Thermo Sequenase dye terminator cycle sequencing pre-mix kit (Amersham Pharmacia Biotech, Uppsala, Sweden). As primers for sequencing reactions specific oligonucleotides complementary to the vector pGEM-T or primers complementary to the cDNA encoding the GABA_B receptor were used.

The larger PCR fragment was found to correspond to the 3'-part of the GABA_B receptor 1a and 1b cDNA and the smaller fragment which lacked 149 base pairs was found to correspond to the 3'-part of the GABA_B receptors 1c and 1d cDNA identified in Example 3A.

EXAMPLE 4: Cloning and sequencing of cDNA encoding canine GABA_B receptor 1b

5 cDNA encoding the canine GABA_B receptor 1b is isolated in a similar manner as described in Example 2 for receptor 1a. PCR primers specifically designed to be complementary to the 5'-end of the cDNA encoding the rat and human GABA_B receptor 1b, together with PCR primers complementary to the 3'-end of the cDNA encoding the canine GABA_B receptor 1a, and mRNA prepared from a suitable canine tissue, are used.

10

EXAMPLE 5: Cloning of cDNA encoding canine GABA_B receptor 1c

Total RNA from canine liver was prepared using the RNeasy Total RNA Purification
15 Protocols (Quiagen GmbH, Germany). The first-strand cDNA synthesis was performed using the First-strand cDNA Synthesis kit from (Amersham Pharmacia Biotech, Uppsala, Sweden). The pd(N)₆ primer was used to prime the first -strand synthesis. The generated cDNA molecules were used as templates in the PCR reaction described below.

20 Specific PCR primers (Table 9) were designed based on the sequence of canine GABA_B receptor 1a cDNA.

TABLE 9**Primers used in RT-PCR**

25

Nr	Species	Sequence 5'-3'	SEQ ID NO
936	canine	CTACCGCGCAATGAACTCCTCGTC	42
954	canine	CCTTCTTCTCCTCCTTCTTAGTGA	43

cDNA fragments encoding parts of the canine GABA_B receptor were amplified directly by PCR using canine specific primers. All PCR experiments were carried out using the Perkin Elmer Taq DNA polymerase with Gene Amp (Roche Molecular Systems Inc., NJ, USA)
30 with the following PCR program: +95°C for 1 minute, +54°C for 30 seconds, +72°C for 3

minutes, repeated 44 times and finally +72°C for 7 minutes. The primer combination gave a PCR product with a size corresponding to the GABA_B receptor 1a but also a fragment of smaller size indicating the presence of a GABA_B receptor 1c.

- 5 The PCR products were subcloned into the pGEM-T vector from Promega (Madison, USA). The inserts were subjected to nucleotide sequence analysis, the complete nucleotide sequence for all subclones were determined using a Thermo Sequenase dye terminator cycle sequencing pre-mix kit (Amersham Pharmacia Biotech, Uppsala, Sweden). As primers for sequencing reactions specific oligonucleotides complementary to the vector
10 pGEM-T were used.

The smaller fragment was shown to lack 149 base pairs. This deletion caused a frame shift and an insertion of a new termination codon, verifying the existence of a canine GABA_B receptor 1c.

15

Complete cDNA sequence encoding the canine GABA_B receptor 1c (SEQ ID NO: 58) was obtained by aligning the sequences of the fragments obtained in Example 2A, Example 2B and Example 5.

20

EXAMPLE 6. Cloning, sequencing and organization of human GABA_B receptor genomic fragments

- To determine the structural organization and sequence of the human GABA_B receptor gene,
25 human genomic DNA libraries and human genomic DNA were screened and analyzed. Human genomic libraries were obtained from Clontech (Palo Alto, CA, USA). The libraries were constructed from female leukocyte DNA (catalog # HL1111J), cloned into λEMBL-3 vector. The average size of inserts are 16 kb and the number of independent clones are 1.7×10^6 . Human genomic DNA was obtained from Clontech (catalog # 6550-1).
30 In order to isolate recombinant phages containing exon and intron sequences of the human GABA_B receptor gene, 48 individual bacterial plates with a diameter of 150 mm and approximately 4×10^4 individual plaques per plate, were screened. The methods and

solutions used were as described in the Library Protocol Handbook: General Procedures for the Hybridization of Lambda Phage Libraries w/DNA Probes (Clontech) with some modifications as will be apparent from the following.

- 5 The experiment was carried out essentially as follows. The numbers are given per plate basis. A sample of the phage library diluted in 0.1 ml sterile lambda diluent was prepared in order to obtain an estimated titer of 40,000 pfu (plaque forming units). A 0.6 ml LB-medium culture of the *E. coli* host strain K802 (obtained from Clontech) was infected with 40000 pfu recombinant phages for 15 minutes at +37°C. The culture was then mixed with
10 7 ml top agarose (6.5 g of agarose added per liter LB) and poured onto LB plates. The plates were incubated at +37°C for approximately 7 hours. The plates were then chilled at +4°C.

- Plaque hybridization experiments were as follows. Membrane filters, Colony/Plaque
15 Screen (DuPont, Wilmington, DE, USA), were placed onto the top of the plates for 3 minutes. For denaturation of DNA the filters were removed and floated in 0.5 M NaOH on a plastic wrap for 2 minutes, with the plaque side up. This step was repeated once to ensure efficient denaturation. Following neutralization the membrane filters were placed in 1M Tris-HCl pH 7.5, two times 2 minutes and allowed to dry.

- 20 To obtain probes for DNA hybridization screening of the membrane filters, a GABA_B receptor cDNA clone was digested with SacII and a 479 bp fragment (base pairs 573-1051 in the cDNA encoding human GABA_B receptor 1a, SEQ ID NO: 48) was separated by agarose electrophoresis, excised and transferred to a polypropylene microcentrifuge tube.
25 Additional probes were obtained by PCR amplification of various regions of the GABA_B receptor cDNA (base pairs 68-486 and 2368-2863 in the cDNA encoding human GABA_B receptor 1a, SEQ ID NO: 48). The isolated cDNA fragment was ³²P-labeled using Megaprime DNA labeling system (Amersham Pharmacia Biotech, Uppsala, Sweden) by the following procedure. Water was added at a ratio of 3 ml per gram of gel, and placed in
30 a boiling water bath for 7 minutes to melt the gel and denature the DNA. A volume of DNA/agarose solution containing 25 ng of DNA was added to the labeling reaction, according to the supplier's instructions. Labeled nucleotides were removed from DNA

labeling reactions using MicroSpin™ G-50 Columns (Amersham Pharmacia Biotech, Uppsala, Sweden).

The DNA hybridization reaction was performed under stringent conditions according to the method described below. The filter membranes were prehybridized at +65°C for at least 1 hour in a solution composed of 1% SDS, 1M NaCl, and 10% dextran sulfate using a hybridization oven (Hybaid Ltd, Ashford, UK). Following prehybridization a solution containing denatured herring sperm DNA of a final concentration of 100 µg/ml and the ³²P-labeled DNA probe at a concentration <10 ng/ml (for optimal signal to background ratio) was added to the prehybridization solution and the membrane filters were incubated at +65°C for 10-20 hours. Following the removal of the hybridization solution the membrane filters were first washed in a 2xSSC (0.3M NaCl, 0.03M Na-citrate), 1% SDS solution two times for 5 minutes at room temperature. In the next step, the membrane filters were incubated +60°C two times for 30 minutes each in the same solution. In a third step, the filters were washed two times at room temperature in 0.1xSSC. Finally, the membrane filters were placed on a sheet of filter paper with the DNA face up, and allowed to dry. The dried membrane filters were then exposed to X-ray films and autoradiographed.

Of the approximately 2x10⁶ individual plaques analyzed, four hybridizing plaques were detected and isolated. These three isolates were designated #GR1, #GR12, #GR13 and #GR41, respectively. After several rescreening experiments, the recombinant phage DNA was purified using Qiagen Lambda Midi Kit (Qiagen GmbH, Germany). The purified DNA was digested with SalI and the fragments representing the inserts were isolated by agarose electrophoresis.

The sizes of the inserts were approximately isolate #GR1, 12 kb, isolate #GR12, 12 kb; isolate #GR13, 16kb; and isolate #GR41, 19 kb. These fragments were cloned into SalI digested linearized pUC19, resulting in the plasmids pAM362 (isolate #GR1), pAM363 (isolate #GR12), pAM364 (isolate #GR13) and pAM365 (isolate #GR41). The inserts from the four plaques which hybridizes to the GABA_B receptor cDNA probes were analyzed by PCR, restriction mapping and hybridization to ³²P-labeled DNA fragments representing various regions of the GABA_B receptor gene.

The cloned fragments in the plasmids pAM362, pAM363, pAM364 and pAM365 were characterized by restriction enzyme mapping, using EcoRI, HindIII, PstI, and BamHI. The approximate positions of the exons and the approximate size of the introns were analyzed and determined by PCR-based exon-exon linking and agarose gel electrophoresis.

In order to facilitate nucleotide sequence analysis, 7 restriction sub-fragments derived from pAM364, 2 restriction fragments derived from pAM362, and 1 restriction sub-fragment derived from pAM365 were isolated and cloned into pUC19, resulting in the plasmids pAM366-pAM375. The following strategy was employed; by combining PCR primers located within the pUC19 sequence either upstream or downstream of the cloning site, with a PCR primer with defined orientation and specific for the GABA_B receptor derived subcloned fragment allowed the determination.

The inserts in the 10 plasmids pAM366-pAM375 were subjected to nucleotide sequence analysis. The nucleotide sequences for all subclones were determined using a Thermo Sequenase dye terminator cycle sequencing pre-mix kit (Amersham Pharmacia Biotech, Uppsala, Sweden). As primers for sequencing reactions specific oligonucleotides complementary to pUC19 or primers complementary to the GABA_B receptor cDNA were used.

The genomic fragments cloned in the plasmids pAM362-pAM365 were shown to contain the complete transcribed part of the human GABA_B receptor gene and extends > 3kb upstream of the first exon and > 2kb downstream of the last exon. The fragments cloned in the plasmid pAM362 were shown to contain exons 7-11, pAM363 exons 12-22, pAM364 exons 1-11, and pAM365 exons 12-23 of the GABA_B receptor gene (Figure 1). The sequence of exons 1-11 and introns 1-10 is listed in SEQ ID NO: 60 and the sequence of exons 12-23 and introns 12-22 is listed in SEQ ID NO: 61.

The human GABA_B receptor gene consists of 23 exons and 22 introns (Figure 1). The size of the exons range between 21 bp and 1486 bp. As can be noted from Table 10 exon/intron boundaries are in accordance with the AG/GT rule and conform well to the consensus sequence suggested by Mount et al. 1982.

TABLE 10

Exon-Intron boundaries of the GABA_B receptor gene, sequences at exon-intron junctions.

		5' splice donor	3' splice acceptor	
Exon 1-Exon 2	CGAG	<u>GTAAGAG</u> <u>CCGCCTCTCACTTAG</u>	ATGT
Exon 2-Exon 3	GAAG	<u>GTGCATC</u> <u>CGACTCACCCCTTAG</u>	GTTG
Exon 3-Exon 4	TGTG	<u>GTGAGTA</u> <u>CCWATCTCTCCACAG</u>	TCCG
Exon 4-Exon 5	CAGG	<u>GTGAGGG</u> <u>CTTTCCTGCTGCCAG</u>	TGAA
Exon 5-Exon 6	TCAG	<u>GTGAGAT</u> <u>CGCACCCCTCCTCAG</u>	AACG
Exon 6-Exon 7	CAAG	<u>GTAGCCC</u> <u>CCTCTTGTCTTTCAG</u>	TGTG
Exon 7-Exon 8	TGTG	<u>GTAAGCA</u> <u>CTCCCTGCCCCACAG</u>	CTTT
Exon 8-Exon 9	TTCG	<u>GTGAGGA</u> <u>TTATTCCCACCCAAG</u>	ACTC
Exon 9-Exon10	GAAG	<u>GTCAGAT</u> <u>CTTTCTCTGTGKTAG</u>	CGCC
Exon10-Exon11	TGAG	<u>GTGGART</u> <u>CTCCTCTGTATTCAG</u>	GTGT
Exon11-Exon12	CATG	<u>GTGAGAG</u> <u>TTTTTTCCTCCCAAG</u>	ACAT
Exon12-Exon13	CTCT	<u>GTGAGTT</u> <u>TGTTCTTCCCTCAG</u>	GGCC
Exon13-Exon14	CAGG	<u>GTTAGTA</u> <u>TTGTCGTCTGCCCAG</u>	GTGG
Exon14-Exon15	ATTG	<u>GTGAGTG</u> <u>CCCTGTGCCATGCAG</u>	GAGG
Exon15-Exon16	TCCG	<u>GTGAGTT</u> <u>CCACCTCTGCCCTAG</u>	TTAT
Exon16-Exon17	CCAG	<u>GTGAGGA</u> <u>TCTCTTCCTTCTAG</u>	GCCC
Exon17-Exon18	GAAG	<u>GTGAGCT</u> <u>CACATATTTATCCAG</u>	ACTC
Exon18-Exon19	TGAG	<u>GTACCAC</u> <u>TYGTTTCTGCCCTAG</u>	ACAT
Exon19-Exon20	CTTG	<u>GTGTGTG</u> <u>CTCCTGCCATCCTAG</u>	GCAT
Exon20-Exon21	GGCA	<u>GTGAGCA</u> <u>TGTCCTTCCCTCTAG</u>	GTCC
Exon21-Exon22	CAAG	<u>GTAAGGA</u> <u>AACATTTGCCCCCAG</u>	ATGC
Exon22-Exon23	TGAG	<u>GTGCGGG</u> <u>TGCTTCTTCCTCCAG</u>	AAAG

5

A comparison of the sequences of the different forms of the human GABA_B receptor cDNA (SEQ ID NO: 48, 50, 54, and 56) and the sequence of the human GABA_B gene (SEQ ID NO: 60 and 61) reveals that different mRNA encoding human GABA_B receptors are formed by alternative splicing. The translational start of the GABA_B receptor 1a is localized in exon 2 and the translational stop is localized in exon 23. The mRNA encoding GABA_B receptor 1b is formed by alternative splicing where part of intron 5 is retained together with exon 6 where the translational start of the GABA_B receptor 1b is derived from the intron sequence. The mRNA encoding GABA_B receptor 1c is formed by alternative splicing where exon 15 are removed together with introns 14 and 15 and a frame shift and a translational stop are generated in the sequence corresponding to exon 16.

10

15

The mRNA encoding GABA_B receptor 1d is formed when the translational start of the GABA_B receptor 1b is generated together with the translational stop of the GABA_B receptor 1c.

- 5 The 1a isoform is formed by splicing exon 5 to a cryptic splice site in the middle of exon 6. Transcription of 1b isoform mRNA is most likely initiated from regulatory elements in intron 5. The ATG initiating translation of 1b mRNA is located in the 5'-end of exon 6.

- 10 Additional variants of the mRNA encoding variants of the human GABA_B receptor can be derived by alternative splicing where one or more of the exons or part of exons are excised in the processing of the pre-mRNA. The subsequent transcription of these mRNA will give rise to variants of the human GABA_B receptor with potentially different biological and/or pharmacological activities.

15

EXAMPLE 7. Analysis of cDNA encoding human GABA_B receptors from human brain

- Messenger RNA from human fetal brain (catalog #6525-1) and adult human brain (catalog #6516-1) were obtained from Clontech (Palo Alto, CA, USA). First strand cDNA synthesis
20 reactions were performed using the first strand cDNA Synthesis kit from Amersham Pharmacia Biotech (Uppsala, Sweden). The pd(N)₆ primer was used to prime the first-strand synthesis. The generated cDNA molecules were used as templates in the PCR reactions described below.

- 25 Specific PCR primers were designed (Table 11) based on the sequences of the rat GABA_B receptor 1a and 1b cDNA and human GABA_B receptor 1a and 1b cDNA

TABLE 11

Primers used for RT-PCR on mRNA from human fetal brain

Nr	Species	Sequence 5'-3'	SEQ ID NO
838	Rat	ATGCGCGCCGGCAGCCAACATGCTGCTGCTGCTGCTGGTGCCTCTCTTCC	62
863	Rat	GGTCATCCAGCGTTGAGGTGAAGAC	63
864	Rat	GAAGGTTGCCAGATTATACATCCGC	64
865	Rat	CCACGATGATTGAGCATCTTGACG	65
937	Human	CTGGTTCCTCCCAATGTG	66
1015	Human	CCAGTGGACTATGAGATTGAG	67

- 5 cDNA fragments encoding parts of the human GABA_B receptors were amplified directly by PCR using the designed primers with the generated cDNA molecules as templates. PCR experiments with primers 838, 863, 864 and 865 were carried out using the Perkin Elmer Taq DNA polymerase with Gene Amp (Roche Molecular System Inc., NJ, USA) with the following PCR program: +95°C for 1 minute, +50°C for 30 seconds, +72°C for 3 minutes, repeated 44 times and finally +72°C for 7 minutes. PCR experiments with primers 937 and 1015 were carried out using the Expand Long Template PCR System (Boehringer Mannheim GmbH, Germany) with the following PCR program: +94°C for 2 minutes; +94°C for 10 seconds, +55°C for 30 seconds, +68°C for 3 minutes repeated 35 times; and finally +68°C for 7 minutes. The primer combinations 838 and 863, 864 and 863, 864 and 865, 937 and 1015 gave PCR products.

The PCR products were subcloned into the pGEM-T vector from Promega (Madison, WI, USA). The inserts were subjected to nucleotide sequence analysis. The complete nucleotide sequence for all subclones were determined using a ThermoSequenase dye terminator cycle sequencing pre-mix kit (Amersham Pharmacia Biotech, Uppsala, Sweden). As for primers for sequencing reactions specific oligonucleotides complementary to the vector pGEM-T or primers complementary to the cDNA encoding the GABA_B receptor were used.

A number of analyzed clones isolated from fetal brain were found to lack 186 base pairs, corresponding to exon 4. This alternative splicing resulted in a cDNA (SEQ ID NO: 70)

encoding a protein (SEQ ID NO: 71) comprising of 899 amino acids and designated GABA_B receptor 1e.

Other clones from fetal brain lacked 368 base pairs, corresponding to exons 4, 5 and 6, resulting in a cDNA (SEQ ID NO: 72) where a frame shift and a translational stop codon are generated in the sequence corresponding to exon 7, encoding a protein (SEQ ID NO: 73) comprising only 97 amino acids designated GABA_B receptor 1f.

One clone lacked 207 base pairs, corresponding to exons 4 and 5, resulting in a cDNA (SEQ ID NO: 74) encoding a protein (SEQ ID NO: 75) comprising 892 amino acids designated GABA_B receptor 1g.

Another clone had two deletions, the first comprising 186 base pairs corresponding to exon 4, the second comprising 39 base pairs corresponding to part of exon 6, resulting in a cDNA (SEQ ID NO: 76) encoding a protein (SEQ ID NO: 77) comprising 886 amino acids designated GABA_B receptor 1h.

Yet another clone from adult human brain was found to have a long deletion comprising 1194 base pairs corresponding to base pairs 319 - 1512 of the cDNA encoding human GABA_B receptor 1a. This deletion corresponds to part of exon 4, exons 5-11, and part of exon 12. This cDNA (SEQ ID NO: 78) encodes a protein (SEQ ID NO: 79) comprising 563 amino acids designated GABA_B receptor 1i.

One clone isolated from fetal brain lacked 284 base pairs corresponding to part of exon 3 and the whole exon 4, generating a frame shift and a translational stop codon in the sequence corresponding to exon 5. This cDNA (SEQ ID NO: 80) encodes a protein (SEQ ID NO: 81) comprising only 105 amino acids designated GABA_B receptor 1j.

EXAMPLE 8. Analysis of cDNA encoding human GABA_B receptors from Jurkat cells

A guanidinisothiocyanate/CsCl method was used to isolate total RNA from Jurkat cells. First strand cDNA synthesis reactions were performed using the first strand cDNA

Synthesis kit from Amersham Pharmacia Biotech (Uppsala, Sweden). The pd(N)₆ primer was used to prime the first-strand synthesis. The generated cDNA molecules were used as templates in the PCR reactions described below.

- 5 Specific PCR primers was designed (Table 12) based on the sequences of the human GABA_B receptor 1a and 1b cDNA

TABLE 12

Primers used for RT-PCR on mRNA from Jurkat cells

10

Nr	Species	Sequence 5'-3'	SEQ ID NO
937	Human	CTGGTTCCTCCCAATGTG	68
1015	Human	CCAGTGGACTATGAGATTGAG	69

cDNA fragments encoding parts of the human GABA_B receptors were amplified directly by PCR using the designed primers with the generated cDNA molecules as templates. The PCR experiment was carried out using the Expand Long Template PCR System

- 15 (Boehringer Mannheim GmbH, Germany) with the following PCR program: +94°C for 2 minutes; +94°C for 10 seconds, +55°C for 30 seconds, +68°C for 3 minutes repeated 35 times; and finally +68°C for 7 minutes. The primer combination 937 and 1015 gave a PCR product.

- 20 The PCR products were subcloned into the pGEM-T vector from Promega (Madison, WI, USA). The inserts were subjected to nucleotide sequence analysis. The complete nucleotide sequence for all subclones were determined using a ThermoSequenase dye terminator cycle sequencing pre-mix kit (Amersham Pharmacia Biotech, Uppsala, Sweden). As for primers for sequencing reactions specific oligonucleotides complementary to the vector pGEM-T or
- 25 primers complementary to the cDNA encoding the GABA_B receptor were used.

Two clones had two deletions, the first comprising 368 base pairs corresponding to exons 4, 5 and 6, the second comprising 151 base pairs corresponding to exon 15 where a frame shift and a translational stop codon are generated in the sequence corresponding to exon 7.

- 30 This cDNA (SEQ ID NO: 82) encodes a protein (SEQ ID NO: 83) comprising only 98

amino acids designated GABA_B receptor 1k which is identical to the GABA_B receptor 1f described above.

Another two clones also had two deletions, the first comprising 246 base pairs

- 5 corresponding to part of exon 4, exon 5 and exon 6, the second comprising 149 base pairs corresponding to exon 15, generating a frame shift and a translational stop codon in the sequence corresponding to exon 16. This cDNA (SEQ ID NO: 84) encodes a protein (SEQ ID NO: 5) comprising 496 amino acids designated GABA_B receptor 1l.

- 10 Additional variants of cDNA encoding the human GABA_B receptors can be identified in a similar manner using PCR primers based on the sequence of the cDNA and genomic fragments encoding the human GABA_B receptors disclosed in the present application.

- The biological activity of these variants of the human GABA_B receptor can be evaluated by
15 transfection of suitable host cells with expression vectors comprising the corresponding cDNA sequences and subsequent measurement of binding of labeled ligands or activation of the receptor or modulation of receptor function.

20 EXAMPLE 9: Generation of antibodies

- Antibodies were raised in rabbits against four different BSA-conjugated 20 amino acids long synthetic peptides corresponding to selected regions of the human and canine GABA_B receptor extracellular domain. Two were directed against a sequence common for GABA_B receptor 1a and b (ab1 and ab2), one against a GABA_B receptor 1a-specific region (a1) and
25 one against a GABA_B receptor 1b-specific sequence (b1). To allow BSA-conjugation, a cystein residue was added to the N-terminus in all peptides but a1, which contains an endogenous cystein.

- 30 Peptide a1: (SEQ ID NO: 49 amino acids 18-37)

Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile Ile His Pro Pro Trp

Peptide ab1: (SEQ ID NO: 49 amino acids 197-216 with N-terminally added Cys)

Cys - Glu Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp Tyr Glu Leu Lys Leu Ile
His His

5 Peptide ab2: (SEQ ID NO: 49 amino acids 271-290 with N-terminally added Cys)

Cys - Ser Pro Ala Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro
Ser Ala

Peptide b1: (SEQ ID NO: 57 amino acids 30-47 with N-terminally added Cys)

10 Cys - Ser His Ser Pro His Leu Pro Arg Pro His Ser Arg Val Pro Pro His Pro Ser

The antibodies were purified from rabbit serum by affinity chromatography using the
corresponding immobilized peptide and subsequently used to detect expression of
recombinant GABA_B receptor isoforms on Western blots.

15

EXAMPLE 10: Heterologous expression of GABA_B receptor isoforms in mammalian cells

A HindIII / Sall cDNA fragment encoding the human GABA_B receptor 1b isoform was
20 cloned into a BPV (bovine papilloma virus)-based expression vector containing the mMT-
1 (murine metallothioneine) promoter. Using the calcium phosphate method, murine C127
cells were co-transfected with the GABA_B receptor expression construct and an expression
plasmid containing a G418 resistance marker gene using the calcium phosphate method.
G418 resistant clones were evaluated by Western blot analysis for expression of the
25 approximately 100 kDa GABA_B receptor 1b isoform (Figure 2). Similarly, but using
Lipofectamine (Life Technologies Inc, Rockville, MD, USA) for transfection, the human
GABA_B receptor 1b isoform was expressed in human HEK-293 cells using the pCI-neo
expression vector. The identity of the heterologously expressed receptor was verified in
HEK-293 cells by Western blot analysis and radioligand binding experiments.

30

A cDNA fragment encoding the human GABA_B receptor 1d isoform was cloned into a
BPV-based expression vector containing the mMT-1 promoter. Using the calcium
phosphate method, murine C127 cells were co-transfected with the GABA_B receptor

expression construct and an expression plasmid containing a G418 resistance marker gene. G418 resistant clones, and concentrated medium from the same clones, were evaluated for GABA_B receptor 1d isoform expression by Western blot analysis (Figure 3). The experiment revealed the human GABA_B receptor 1d to be a secreted isoform.

5

EXAMPLE 11: Heterologous expression of GABA_B receptor isoforms in *E. coli*

A cDNA fragment encoding the human GABA_B receptor 1d isoform was cloned into a modified pET (Pharmacia Amersham, Uppsala, Sweden) vector downstream of a STII (heat stable enterotoxin II of *E. coli*) signal peptide and followed by a thrombin cleavage site and a hexahistidine tag. The expression construct was subsequently used to transform the BL21 (DE3) *E. coli* strain. Western blot analysis of IPTG-induced bacteria revealed expression of a human GABA_B receptor 1d isoform of expected size (Figure 4).

15

In addition, the human GABA_B receptor 1d isoform was successfully expressed without fusion to a bacterial signal peptide in *E. coli* strain AD494 (DE3).

EXAMPLE 12: Method for the screening of substances which are GABA_B receptor antagonists or agonists

GABA_B receptor expressing cells, transgenic animals or cells and tissues derived thereof, are used to screen substance libraries for antagonist or agonist activities. Screening is performed as ligand binding assays or functional assays. For screening, cells and tissues are prepared in various ways, each uniquely suited to its purpose. Ligand binding assays are performed *in vivo* or *in vitro*. Functional assays exemplified by, but not limited to, Ca⁺⁺-responses, cAMP-responses and effects on Cl⁻ and K⁺ channels, are performed in living cells, broken cells, isolated cell membranes, as well as in tissues and in living animals.

25

CLAIMS

1. A nucleic acid molecule encoding a human or canine GABA_B receptor, or a functionally equivalent modified form thereof.
2. A nucleic acid molecule according to claim 1 encoding a human GABA_B receptor, or a functionally equivalent modified form thereof.
3. A nucleic acid molecule according to claim 2 encoding the human GABA_B receptor 1a, or a functionally equivalent modified form thereof.
4. A nucleic acid molecule according to claim 3 selected from:
 - (a) a nucleic acid molecule comprising a nucleotide sequence set forth as SEQ ID NO: 48;
 - (b) a nucleic acid molecule comprising a nucleotide sequence capable of hybridizing, under stringent hybridization conditions, to a nucleotide sequence complementary to the polypeptide coding region of a DNA molecule as defined in (a); and
 - (c) a nucleic acid molecule comprising a nucleotide sequence which is degenerate as a result of the genetic code to a nucleotide sequence as defined in (a) or (b).
5. A nucleic acid molecule according to claim 2 encoding the human GABA_B receptor 1b, or a functionally equivalent modified form thereof..
6. A nucleic acid molecule according to claim 5 selected from:
 - (a) nucleic acid molecules comprising a nucleotide sequence set forth as SEQ ID NO: 50;
 - (b) nucleic acid molecules comprising a nucleotide sequence capable of hybridizing, under stringent hybridization conditions, to a nucleotide sequence complementary the polypeptide coding region of a DNA molecule as defined in (a); and
 - (c) nucleic acid molecules comprising a nucleotide sequence which is degenerate as a result of the genetic code to a nucleotide sequence as defined in (a) or (b).

7. A nucleic acid molecule according to claim 2 encoding the human GABA_B receptor 1c, or a functionally equivalent modified form thereof.
8. A nucleic acid molecule according to claim 7 selected from:
- 5 (a) nucleic acid molecules comprising a nucleotide sequence set forth as SEQ ID NO: 54;
- (b) nucleic acid molecules comprising a nucleotide sequence capable of hybridizing, under stringent hybridization conditions, to a nucleotide sequence complementary the polypeptide coding region of a DNA molecule as defined in (a); and
- 10 (c) nucleic acid molecules comprising a nucleotide sequence which is degenerate as a result of the genetic code to a nucleotide sequence as defined in (a) or (b).
9. A nucleic acid molecule according to claim 2 encoding the human GABA_B receptor 1d, or a functionally equivalent modified form thereof..
- 15 10. A nucleic acid molecule according to claim 9 selected from:
- (a) nucleic acid molecules comprising a nucleotide sequence set forth as SEQ ID NO: 56;
- (b) nucleic acid molecules comprising a nucleotide sequence capable of hybridizing, under stringent hybridization conditions, to a nucleotide sequence complementary the polypeptide coding region of a DNA molecule as defined in (a); and
- 20 (c) nucleic acid molecules comprising a nucleotide sequence which is degenerate as a result of the genetic code to a nucleotide sequence as defined in (a) or (b).
- 25 11. A nucleic acid molecule according to claim 1 encoding a canine GABA_B receptor, or a functionally equivalent modified form thereof.
12. A nucleic acid molecule according to claim 11 encoding the canine GABA_B receptor 1a, or a functionally equivalent modified form thereof.
- 30 13. A nucleic acid molecule according to claim 12 selected from

(a) nucleic acid molecules comprising a nucleotide sequence set forth as SEQ ID NO: 52;

(b) nucleic acid molecules comprising a nucleotide sequence capable of hybridizing, under stringent hybridization conditions, to a nucleotide sequence complementary the polypeptide coding region of a DNA molecule as defined in (a); and

(c) nucleic acid molecules comprising a nucleotide sequence which is degenerate as a result of the genetic code to a nucleic acid sequence as defined in (a) or (b).

14 A nucleic acid molecule according to claim 11 encoding the canine GABA_B receptor 1c, or a functionally equivalent modified form thereof.

15. A nucleic acid molecule according to claim 14 selected from

(a) nucleic acid molecules comprising a nucleotide sequence set forth as SEQ ID NO: 58;

(b) nucleic acid molecules comprising a nucleotide sequence capable of hybridizing, under stringent hybridization conditions, to a nucleotide sequence complementary the polypeptide coding region of a DNA molecule as defined in (a); and

(c) nucleic acid molecules comprising a nucleotide sequence which is degenerate as a result of the genetic code to a nucleic acid sequence as defined in (a) or (b).

16. A recombinant polypeptide encoded by a nucleotide sequence according to any one of claims 1 to 15.

17. The polypeptide according to claim 16 comprising an amino acid sequence set forth as SEQ ID NO: 49, 51, 53, 55, 57 or 59 in the Sequence Listing.

18. A polypeptide according to claim 16 which has been posttranslationally modified.

19. A vector transformed with a nucleic acid molecule according to any one of claims 1 to 15.

20. A cultured host cell harboring a vector according to claim 19.

21. A process for the production of a GABA_B receptor, said process comprising culturing a host cell according to claim 20 under conditions whereby the said polypeptide is produced, and recovering the said polypeptide.
- 5
22. A method for the screening of compounds which are inhibitors of transient lower esophageal sphincter relaxations, said method comprising the use of a nucleic acid molecule encoding a GABA_B receptor.
- 10
23. A method according to claim 22 wherein the said nucleic acid molecule encoding a GABA_B receptor is the nucleic acid molecule according to any one of claims 1 to 15.
24. A method for the screening of compounds which are agonists or antagonists to a GABA_B receptor, said method comprising the use of a nucleic acid molecule
- 15
- according to any one of claims 1 to 15.
25. A method according to any one of claims 22 to 24 comprising the steps (a) transforming a cultured cell with a nucleic acid molecule encoding a GABA_B receptor, so that a GABA_B receptor is expressed on the surface of the cell; (b)
- 20
- contacting a test compound with the said cell; and (c) determining whether the test compound binds to, and/or activate, the GABA_B receptor.
26. A pharmaceutical compositions comprising a soluble GABA_B receptor further comprising one or more pharmaceutical acceptable carriers and/or diluents.

1/2

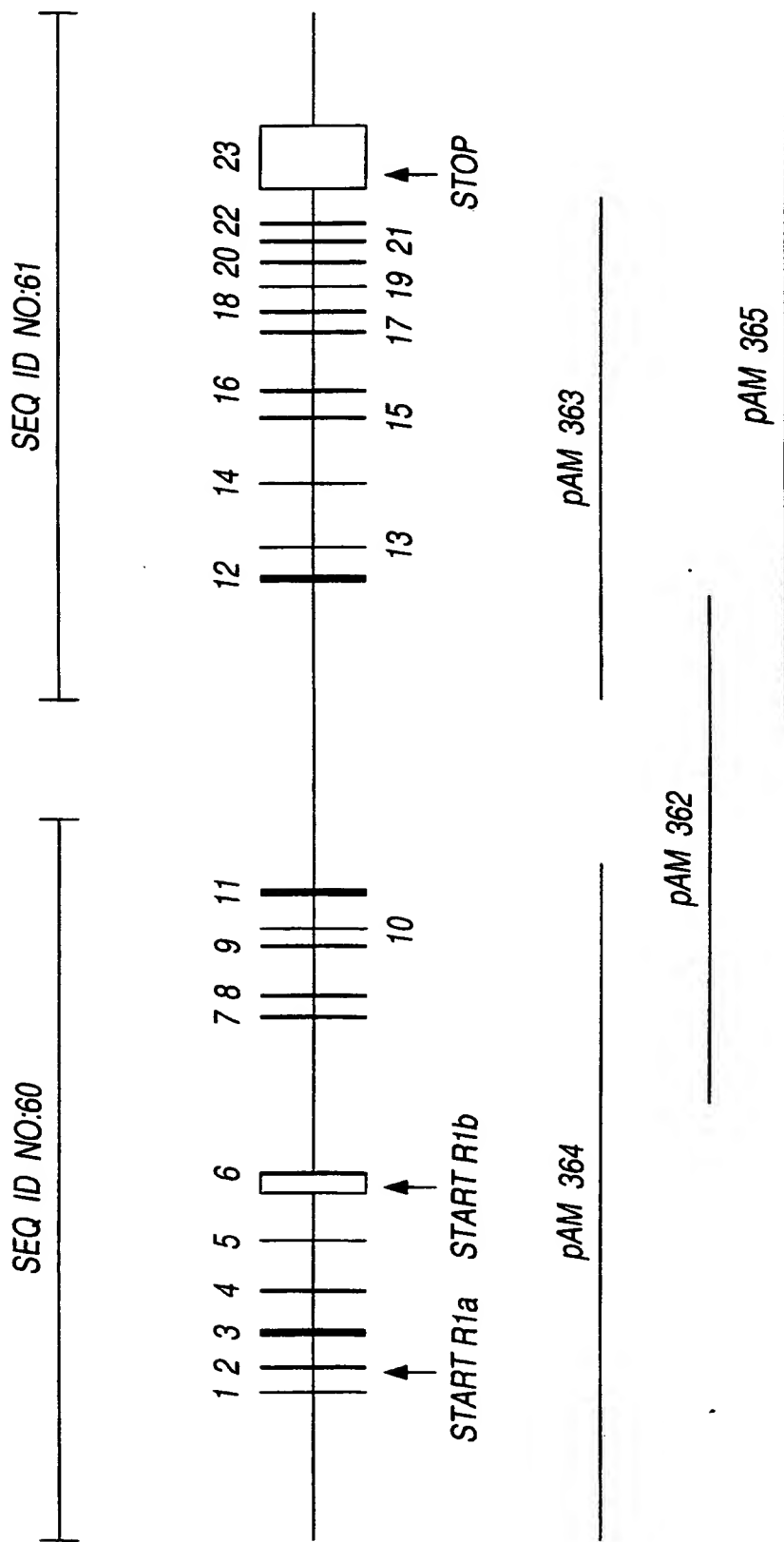


Fig.1

2/2

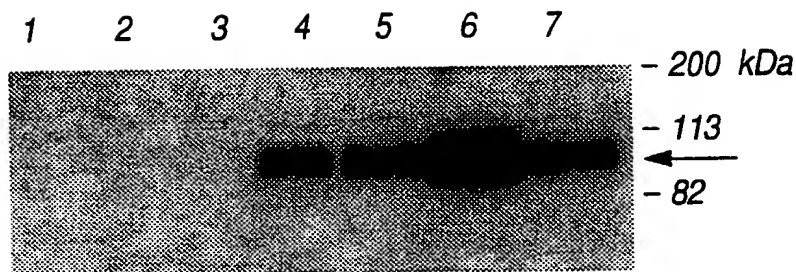


Fig.2

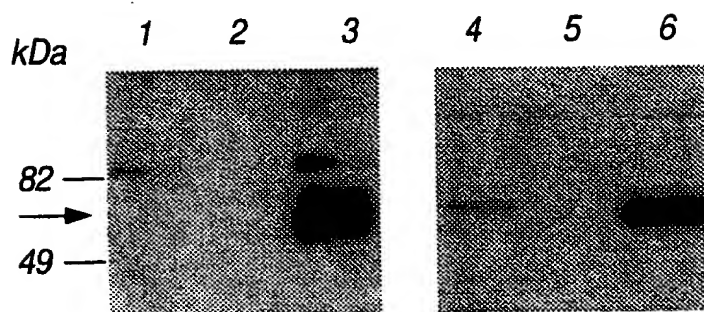


Fig.3

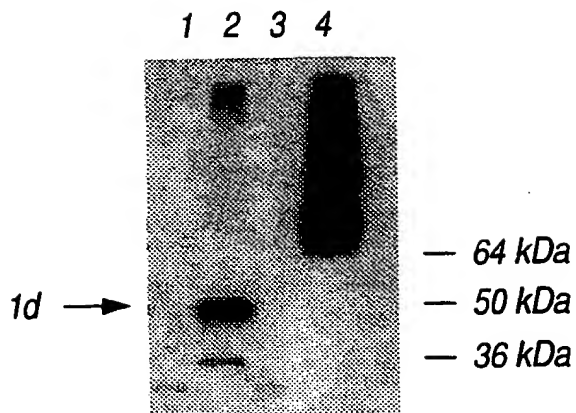


Fig.4

SEQUENCE LISTING

5

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: ASTRA AB
(B) STREET: Västra Mälarehamnen 9
(C) CITY: Södertälje
(E) COUNTRY: Sweden
(F) POSTAL CODE (ZIP): S-151 85
(G) TELEPHONE: +46-8-553 260 00
(H) TELEFAX: +46-8-553 288 20
(I) TELEX: 19237 astra s

15

(ii) TITLE OF INVENTION: New nucleotide sequences

20 (iii) NUMBER OF SEQUENCES: 85

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

25

(2) INFORMATION FOR SEQ ID NO: 1:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

40

GTTTCTTCTC GGATCCAGCT GTGCCTG

27

(2) INFORMATION FOR SEQ ID NO: 2:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

15 CAGGCACAGC TGGATCCGAG AAGAAACT

28

(2) INFORMATION FOR SEQ ID NO: 3:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

30 CGGTCGACTC ACTTGTAAG CAAATGTACT CGACTCCC

38

(2) INFORMATION FOR SEQ ID NO: 4:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ATGCGCGCCG GCAGCCAACA TGCTGCTGCT GCTGCTGGTG C

41

5 (2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CGGTCGACTC ACTTGTAAG CAAATGTACT CGACTCCCAT CACAGC

46

20 (2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

25 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

ATGCGCGCCG GCAGCCAACA TGCTGCTGCT GCTGCTGGTG CCTCTCTTCC

50

35 (2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid

40 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CAGGCACAGC TGGATCCGAG AAGAAACTCT GTCGGAAAGT

40

5

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GGTCATCCAG CGTTGAGGTG AAGAC

25

20

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GAAGGTTGCC AGATTATACA TCCGC

25

35

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

5

CCACGATGAT TCGAGCATCT TGACG

25

(2) INFORMATION FOR SEQ ID NO: 11:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

15

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

20

GCCTTCTACT CCCCTCATCT CC

22

(2) INFORMATION FOR SEQ ID NO: 12:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

30

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

35

GAGTGAAGGA GGCTGGAATT G

21

(2) INFORMATION FOR SEQ ID NO: 13:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

GACGCTTATC GAGCAGCTTC

20

10

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

AGCCCAGAAC TCACAGGGGG ACAT

24

25

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GCTTCAAGCC AGGTACGAAC TAA

23

40

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

TGGCCCTCCA CCGCCTCAGT CATCTCA

27

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CCATCCTAAT ACGACTCACT ATAGGGC

27

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

CTCAATCTCA TAGTCCACTG G

21

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

CCTTGAGGCC CGGGGAGAG

19

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

CAGGCACAGC TGGATCCGAG AAGAAACT

28

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

CGGTCGACTC ACTTGTAAG CAAATGTACT CGACTCCCAT CACAGC

46

(2) INFORMATION FOR SEQ ID NO: 22:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

15 ATGCGCGCCG GCAGCCAACA TGCTGCTGCT GCTGCTGGTG CCTCTCTTCC

50

(2) INFORMATION FOR SEQ ID NO: 23:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

30 CGTCAAGATG CTCGAATCAT CG

22

(2) INFORMATION FOR SEQ ID NO: 24:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 40 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

CAGGGGGCTC AGAGGGTCCC

20

5 (2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

CAGGCACAGC TGGATCCGAG AAGAACTCT GTCGGAAAGT

40

20 (2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- 25 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

CGGTCGACTC ACTTGTAAG CAAATGTACT CGACTCCCAT CACAGCTAAG

50

35 (2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- 40 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

ACTTTCCGAC AGAGTTTCTT CTCGGATCCA GCTGTGCCTG

40

5

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

CCACGATGAT TCGAGCATCT TGACG

25

20

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

CTACCGCGCA ATGAACTCCT CGTC

24

35

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

5

CGAGGTGGCG TTGGGGGTCT GTGC

24

(2) INFORMATION FOR SEQ ID NO: 31:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

15

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

20

CCATCCTAAT ACGACTCACT ATAGGGC

27

(2) INFORMATION FOR SEQ ID NO: 32:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

30

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

35

ACTCACTATA GGGCTCGAGC GGC

23

(2) INFORMATION FOR SEQ ID NO: 33:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

GACGCTTATC GAGCAGCTTC

20

10

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

15

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

AGCCCAGAAC TCACAGGGGG ACAT

24

25

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

30

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

GCTTCAAGCC AGGTACGAAC TAA

23

40

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

10 GGAGCACCCC CAAGCCCCAC TG

22

(2) INFORMATION FOR SEQ ID NO: 37:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

25 CTGGTTCCTC CCAATGTG

18

(2) INFORMATION FOR SEQ ID NO: 38:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

40 CCTCTCACTC CCCTCATCTC

20

(2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: DNA

- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

AAGCCAACCT TCCCTGCTTC TC

22

- 15 (2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: DNA

- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

CTGGTTCCTC CCAATGTG

18

- 30 (2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: DNA

- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GACGCTTATC GAGCAGCTTC

20

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

2

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

CTACCGCGCA ATGAACTCCT CGTC

24

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

CCTTCTTCTC CTCCTTCTTA GTGA

24

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2883 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Rattus norvegicus*

5

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..2883

10

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Kaupmann, K

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15

Bischoff, S

Mickel, S

McMaster, G

Angst, C

Bittiger, H

20

Froestl, W

(B) TITLE: Expression cloning of GABA-B receptors
uncovers similarity to metabotropic glutamate
receptors

(C) JOURNAL: Nature

25

(D) VOLUME: 386

(F) PAGES: 239-246

(G) DATE: 20 march-1997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

30

ATG CTG CTG CTG CTG CTG GTG CCT CTC TTC CTC CGC CCC CTG GGC GCT 48

Met Leu Leu Leu Leu Leu Val Pro Leu Phe Leu Arg Pro Leu Gly Ala

1

5

10

15

35

GGC GGC GCG CAG ACC CCC AAC GCC ACC TCG GAA GGT TGC CAG ATT ATA 96

Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile Ile

20

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CAT CCG CCC TGG GAA GGT GGC ATC AGG TAC CGT GGC TTG ACT CGC GAC 144

His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg Asp

35

40

45

CAG GTG AAG GCC ATC AAC TTC CTG CCT GTG GAC TAT GAG ATC GAA TAT 192

	Gln	Val	Lys	Ala	Ile	Asn	Phe	Leu	Pro	Val	Asp	Tyr	Glu	Ile	Glu	Tyr	
	50						55					60					
	GTG	TGC	CGA	GGG	GAG	CGC	GAG	GTG	GTG	GGG	CCC	AAG	GTG	CGC	AAA	TGC	240
5	Val	Cys	Arg	Gly	Glu	Arg	Glu	Val	Val	Gly	Pro	Lys	Val	Arg	Lys	Cys	
	65					70					75				80		
	CTG	GCC	AAC	GGC	TCC	TGG	ACG	GAT	ATG	GAC	ACA	CCC	AGC	CGC	TGT	GTC	288
10	Leu	Ala	Asn	Gly	Ser	Trp	Thr	Asp	Met	Asp	Thr	Pro	Ser	Arg	Cys	Val	
				85						90					95		
	CGA	ATC	TGC	TCC	AAG	TCT	TAT	TTG	ACC	CTG	GAA	AAT	GGG	AAG	GTT	TTC	336
	Arg	Ile	Cys	Ser	Lys	Ser	Tyr	Leu	Thr	Leu	Glu	Asn	Gly	Lys	Val	Phe	
				100					105					110			
15	CTG	ACG	GGT	GGG	GAC	CTC	CCA	GCT	CTG	GAT	GGA	GCC	CGG	GTG	GAG	TTC	384
	Leu	Thr	Gly	Gly	Asp	Leu	Pro	Ala	Leu	Asp	Gly	Ala	Arg	Val	Glu	Phe	
				115					120					125			
20	CGA	TGT	GAC	CCC	GAC	TTC	CAT	CTG	GTG	GGC	AGC	TCC	CGG	AGC	GTC	TGT	432
	Arg	Cys	Asp	Pro	Asp	Phe	His	Leu	Val	Gly	Ser	Ser	Arg	Ser	Val	Cys	
		130				135					140						
	AGT	CAG	GGC	CAG	TGG	AGC	ACC	CCC	AAG	CCC	CAC	TGC	CAG	GTG	AAT	CGA	480
25	Ser	Gln	Gly	Gln	Trp	Ser	Thr	Pro	Lys	Pro	His	Cys	Gln	Val	Asn	Arg	
	145				150					155				160			
	ACG	CCA	CAC	TCA	GAA	CGG	CGT	GCA	GTA	TAC	ATC	GGG	GCG	CTG	TTT	CCC	528
30	Thr	Pro	His	Ser	Glu	Arg	Arg	Ala	Val	Tyr	Ile	Gly	Ala	Leu	Phe	Pro	
				165						170				175			
	ATG	AGC	GGG	GGC	TGG	CCG	GGG	GGC	CAG	GCC	TGC	CAG	CCC	GCG	GTG	GAG	576
	Met	Ser	Gly	Gly	Trp	Pro	Gly	Gly	Gln	Ala	Cys	Gln	Pro	Ala	Val	Glu	
				180					185					190			
35	ATG	GCG	CTG	GAG	GAC	GTT	AAC	AGC	CGC	AGA	GAC	ATC	CTG	CCG	GAC	TAC	624
	Met	Ala	Leu	Glu	Asp	Val	Asn	Ser	Arg	Arg	Asp	Ile	Leu	Pro	Asp	Tyr	
				195					200					205			
40	GAG	CTC	AAG	CTT	ATC	CAC	CAC	GAC	AGC	AAG	TGT	GAC	CCA	GGG	CAA	GCC	672
	Glu	Leu	Lys	Leu	Ile	His	His	Asp	Ser	Lys	Cys	Asp	Pro	Gly	Gln	Ala	
				210				215						220			

	ACC AAG TAC TTG TAC GAA CTA CTC TAC AAT GAC CCC ATC AAG ATC ATT	720
	Thr Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile Ile	
	225 230 235 240	
5	CTC ATG CCT GGC TGT AGT TCT GTC TCC ACA CTT GTA GCT GAG GCT GCC	768
	Leu Met Pro Gly Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala Ala	
	245 250 255	
10	CGG ATG TGG AAC CTT ATT GTG CTC TCA TAT GGC TCC AGT TCA CCA GCC	816
	Arg Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro Ala	
	260 265 270	
15	TTG TCA AAC CGA CAG CGG TTT CCC ACG TTC TTC CGG ACG CAT CCA TCC	864
	Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro Ser	
	275 280 285	
20	GCC ACA CTC CAC AAT CCC ACC CGG GTG AAA CTC TTC GAA AAG TGG GGC	912
	Ala Thr Leu His Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp Gly	
	290 295 300	
25	TGG AAG AAG ATC GCT ACC ATC CAA CAG ACC ACC GAG GTC TTC ACC TCA	960
	Trp Lys Lys Ile Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr Ser	
	305 310 315 320	
30	ACG CTG GAT GAC CTG GAG GAG CGA GTG AAA GAG GCT GGG ATC GAG ATC	1008
	Thr Leu Asp Asp Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu Ile	
	325 330 335	
35	ACT TTC CGA CAG AGT TTC TTC TCG GAT CCA GCT GTG CCT GTT AAA AAC	1056
	Thr Phe Arg Gln Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys Asn	
	340 345 350	
40	CTG AAG CGT CAA GAT GCT CGA ATC ATC GTG GGA CTT TTC TAT GAG ACG	1104
	Leu Lys Arg Gln Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu Thr	
	355 360 365	
45	GAA GCC CGG AAA GTT TTT TGT GAG GTC TAT AAG GAA AGG CTC TTT GGG	1152
	Glu Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe Gly	
	370 375 380	
50	AAG AAG TAC GTC TGG TTC CTC ATC GGG TGG TAT GCT GAC AAC TGG TTC	1200
	Lys Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp Phe	
	385 390 395 400	

	AAG ACC TAT GAC CCG TCA ATC AAT TGT ACA GTG GAA GAA ATG ACC GAG	1248
	Lys Thr Tyr Asp Pro Ser Ile Asn Cys Thr Val Glu Glu Met Thr Glu	
	405 410 415	
5	GCG GTG GAG GGC CAC ATC ACC ACG GAG ATT GTC ATG CTG AAC CCT GCC	1296
	Ala Val Glu Gly His Ile Thr Thr Glu Ile Val Met Leu Asn Pro Ala	
	420 425 430	
10	AAC AEC CGA AGC ATT TCC AAC ATG ACG TCA CAG GAA TTT GTG GAG AAA	1344
	Asn Thr Arg Ser Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu Lys	
	435 440 445	
	CTA ACC AAG CGG CTG AAA AGA CAC CCC GAG GAG ACT GGA GGC TTC CAG	1392
15	Leu Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe Gln	
	450 455 460	
	GAG GCA CCA CTG GCC TAT GAT GCT ATC TGG GCC TTG GCT TTG GCC TTG	1440
	Glu Ala Pro Leu Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala Leu	
20	465 470 475 480	
	AAC AAG ACG TCT GGA GGA GGT GGT CGT TCC GGC GTG CGC CTG GAG GAC	1488
	Asn Lys Thr Ser Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu Asp	
	485 490 495	
25	TTT AAC TAC AAC AAC CAG ACC ATT ACA GAC CAG ATC TAC CGG GCC ATG	1536
	Phe Asn Tyr Asn Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala Met	
	500 505 510	
30	AAC TCC TCC TCC TTT GAG GGC GTT TCT GGC CAT GTG GTC TTT GAT GCC	1584
	Asn Ser Ser Ser Phe Glu Gly Val Ser Gly His Val Val Phe Asp Ala	
	515 520 525	
	AGC GGC TCC CGG ATG GCA TGG ACA CTT ATC GAG CAG CTA CAG GGC GGC	1632
35	Ser Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly Gly	
	530 535 540	
	AGC TAC AAG AAG ATC GGC TAC TAC GAC AGC ACC AAG GAT GAT CTT TCC	1680
	Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu Ser	
40	545 550 555 560	
	TGG TCC AAA ACG GAC AAG TGG ATT GGA GGG TCT CCC CCA GCT GAC CAG	1728
	Trp Ser Lys Thr Asp Lys Trp Ile Gly Gly Ser Pro Pro Ala Asp Gln	

	565	570	575	
	ACC TTG GTC ATC AAG ACA TTC CGT TTC CTG TCT CAG AAA CTC TTT ATC			1776
	Thr Leu Val Ile Lys Thr Phe Arg Phe Leu Ser Gln Lys Leu Phe Ile			
5	580	585	590	
	TCC GTC TCA GTT CTC TCC AGC CTG GGC ATT GTT CTT GCT GTT GTC TGT			1824
	Ser Val Ser Val Leu Ser Ser Leu Gly Ile Val Leu Ala Val Val Cys			
	595	600	605	
10	CTG TCC TTT AAC ATC TAC AAC TCC CAC GTT CGT TAT ATC CAG AAC TCC			1872
	Leu Ser Phe Asn Ile Tyr Asn Ser His Val Arg Tyr Ile Gln Asn Ser			
	610	615	620	
15	CAG CCC AAC CTG AAC AAT CTG ACT GCT GTG GGC TGC TCA CTG GCA CTG			1920
	Gln Pro Asn Leu Asn Asn Leu Thr Ala Val Gly Cys Ser Leu Ala Leu			
	625	630	635	640
	GCT GCT GTC TTC CCT CTC GGG CTG GAT GGT TAC CAC ATA GGG AGA AGC			1968
20	Ala Ala Val Phe Pro Leu Gly Leu Asp Gly Tyr His Ile Gly Arg Ser			
	645	650	655	
	CAG TTC CCG TTT GTC TGC CAG GCC CGC CTT TGG CTC TTG GGC TTG GGC			2016
	Gln Phe Pro Phe Val Cys Gln Ala Arg Leu Trp Leu Leu Gly Leu Gly			
25	660	665	670	
	TTT AGT CTG GGC TAT GGC TCT ATG TTC ACC AAG ATC TGG TGG GTC CAC			2064
	Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr Lys Ile Trp Trp Val His			
	675	680	685	
30	ACA GTC TTC ACG AAG AAG GAG GAG AAG AAG GAG TGG AGG AAG ACC CTA			2112
	Thr Val Phe Thr Lys Lys Glu Glu Lys Lys Glu Trp Arg Lys Thr Leu			
	690	695	700	
35	GAG CCC TGG AAA CTC TAT GCC ACT GTG GGC CTG CTG GTG GGC ATG GAT			2160
	Glu Pro Trp Lys Leu Tyr Ala Thr Val Gly Leu Leu Val Gly Met Asp			
	705	710	715	720
	GTC CTG ACT CTT GCC ATC TGG CAG ATT GTG GAC CCC TTG CAC CGA ACC			2208
40	Val Leu Thr Leu Ala Ile Trp Gln Ile Val Asp Pro Leu His Arg Thr			
	725	730	735	
	ATT GAG ACT TTT GCC AAG GAG GAA CCA AAG GAA GAC ATC GAT GTC TCC			2256

	Ile	Glu	Thr	Phe	Ala	Lys	Glu	Glu	Pro	Lys	Glu	Asp	Ile	Asp	Val	Ser	
					740				745						750		
	ATT	CTG	CCC	CAG	TTG	GAG	CAC	TGC	AGC	TCC	AAG	AAG	ATG	AAT	ACG	TGG	2304
5	Ile	Leu	Pro	Gln	Leu	Glu	His	Cys	Ser	Ser	Lys	Lys	Met	Asn	Thr	Trp	
					755				760						765		
	CTT	GGC	ATT	TTC	TAT	GGT	TAC	AAG	GGG	CTG	CTG	CTG	CTG	CTG	GGA	ATC	2352
10	Leu	Gly	Ile	Phe	Tyr	Gly	Tyr	Lys	Gly	Leu	Leu	Leu	Leu	Leu	Gly	Ile	
					770				775						780		
	TTT	CTT	GCT	TAC	GAA	ACC	AAG	AGC	GTG	TCC	ACT	GAA	AAG	ATC	AAT	GAC	2400
	Phe	Leu	Ala	Tyr	Glu	Thr	Lys	Ser	Val	Ser	Thr	Glu	Lys	Ile	Asn	Asp	
					785				790					795		800	
15	CAC	AGG	GCC	GTG	GGC	ATG	GCT	ATC	TAC	AAT	GTC	GCG	GTC	CTG	TGT	CTC	2448
	His	Arg	Ala	Val	Gly	Met	Ala	Ile	Tyr	Asn	Val	Ala	Val	Leu	Cys	Leu	
					805					810					815		
20	ATC	ACT	GCT	CCT	GTG	ACC	ATG	ATC	CTT	TCC	AGT	CAG	CAG	GAC	GCA	GCC	2496
	Ile	Thr	Ala	Pro	Val	Thr	Met	Ile	Leu	Ser	Ser	Gln	Gln	Asp	Ala	Ala	
					820				825						830		
	TTT	GCC	TTT	GCC	TCT	CTG	GCC	ATC	GTG	TTC	TCT	TCC	TAC	ATC	ACT	CTG	2544
25	Phe	Ala	Phe	Ala	Ser	Leu	Ala	Ile	Val	Phe	Ser	Ser	Tyr	Ile	Thr	Leu	
					835				840						845		
	GTT	GTG	CTC	TTT	GTG	CCC	AAG	ATG	CGC	AGG	CTG	ATC	ACC	CGA	GGG	GAA	2592
30	Val	Val	Leu	Phe	Val	Pro	Lys	Met	Arg	Arg	Leu	Ile	Thr	Arg	Gly	Glu	
					850				855					860			
	TGG	CAG	TCT	GAA	ACG	CAG	GAC	ACC	ATG	AAA	ACA	GGA	TCA	TCC	ACC	AAC	2640
	Trp	Gln	Ser	Glu	Thr	Gln	Asp	Thr	Met	Lys	Thr	Gly	Ser	Ser	Thr	Asn	
					865				870					875		880	
35	AAC	AAC	GAG	GAA	GAG	AAG	TCC	CGA	CTG	TTG	GAG	AAG	GAA	AAC	CGA	GAA	2688
	Asn	Asn	Glu	Glu	Glu	Lys	Ser	Arg	Leu	Leu	Glu	Lys	Glu	Asn	Arg	Glu	
					885				890						895		
40	CTG	GAA	AAG	ATC	ATC	GCT	GAG	AAA	GAG	GAG	CGC	GTC	TCT	GAA	CTG	CGC	2736
	Leu	Glu	Lys	Ile	Ile	Ala	Glu	Lys	Glu	Glu	Arg	Val	Ser	Glu	Leu	Arg	
					900				905						910		

CAT CAG CTC CAG TCT CGG CAG CAA CTC CGC TCA CGG CGC CAC CCC CCA 2784
 His Gln Leu Gln Ser Arg Gln Gln Leu Arg Ser Arg Arg His Pro Pro
 915 920 925

5 ACA CCC CCA GAT CCC TCT GGG GGC CTT CCC AGG GGA CCC TCT GAG CCC 2832
 Thr Pro Pro Asp Pro Ser Gly Gly Leu Pro Arg Gly Pro Ser Glu Pro
 930 935 940

CCT GAC CGG CTT AGC TGT GAT GGG AGT CGA GTA CAT TTG CTT TAC AAG 2880
 10 Pro Asp Arg Leu Ser Cys Asp Gly Ser Arg Val His Leu Leu Tyr Lys
 945 950 955 960

TGA 2883
 *

15

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 960 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

Met Leu Leu Leu Leu Leu Val Pro Leu Phe Leu Arg Pro Leu Gly Ala
 1 5 10 15

30 Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile Ile
 20 25 30

His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg Asp
 35 35 40 45

Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu Tyr
 50 55 60

40 Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys Cys
 65 70 75 80

Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys Val

	85	90	95
	Arg Ile Cys Ser Lys Ser Tyr Leu Thr Leu Glu Asn Gly Lys Val Phe		
	100	105	110
5	Leu Thr Gly Gly Asp Leu Pro Ala Leu Asp Gly Ala Arg Val Glu Phe		
	115	120	125
	Arg Cys Asp Pro Asp Phe His Leu Val Gly Ser Ser Arg Ser Val Cys		
10	130	135	140
	Ser Gln Gly Gln Trp Ser Thr Pro Lys Pro His Cys Gln Val Asn Arg		
	145	150	155 160
15	Thr Pro His Ser Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe Pro		
	165	170	175
	Met Ser Gly Gly Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val Glu		
	180	185	190
20	Met Ala Leu Glu Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp Tyr		
	195	200	205
	Glu Leu Lys Leu Ile His His Asp Ser Lys Cys Asp Pro Gly Gln Ala		
25	210	215	220
	Thr Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile Ile		
	225	230	235 240
30	Leu Met Pro Gly Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala Ala		
	245	250	255
	Arg Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro Ala		
	260	265	270
35	Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro Ser		
	275	280	285
	Ala Thr Leu His Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp Gly		
40	290	295	300
	Trp Lys Lys Ile Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr Ser		
	305	310	315 320

Thr Leu Asp Asp Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu Ile
 325 330 335

5 Thr Phe Arg Gln Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys Asn
 340 345 350

Leu Lys Arg Gln Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu Thr
 355 360 365

10 Glu Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe Gly
 370 375 380

Lys Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp Phe
 15 385 390 395 400

Lys Thr Tyr Asp Pro Ser Ile Asn Cys Thr Val Glu Glu Met Thr Glu
 405 410 415

20 Ala Val Glu Gly His Ile Thr Thr Glu Ile Val Met Leu Asn Pro Ala
 420 425 430

Asn Thr Arg Ser Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu Lys
 435 440 445

25 Leu Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe Gln
 450 455 460

Glu Ala Pro Leu Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala Leu
 30 465 470 475 480

Asn Lys Thr Ser Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu Asp
 485 490 495

35 Phe Asn Tyr Asn Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala Met-
 500 505 510

Asn Ser Ser Ser Phe Glu Gly Val Ser Gly His Val Val Phe Asp Ala
 515 520 525

40 Ser Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly Gly
 530 535 540

Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu Ser
 545 550 555 560
 Trp Ser Lys Thr Asp Lys Trp Ile Gly Gly Ser Pro Pro Ala Asp Gln
 5 565 570 575
 Thr Leu Val Ile Lys Thr Phe Arg Phe Leu Ser Gln Lys Leu Phe Ile
 580 585 590
 Ser Val Ser Val Leu Ser Ser Leu Gly Ile Val Leu Ala Val Val Cys
 10 595 600 605
 Leu Ser Phe Asn Ile Tyr Asn Ser His Val Arg Tyr Ile Gln Asn Ser
 610 615 620
 Gln Pro Asn Leu Asn Asn Leu Thr Ala Val Gly Cys Ser Leu Ala Leu
 15 625 630 635 640
 Ala Ala Val Phe Pro Leu Gly Leu Asp Gly Tyr His Ile Gly Arg Ser
 20 645 650 655
 Gln Phe Pro Phe Val Cys Gln Ala Arg Leu Trp Leu Leu Gly Leu Gly
 660 665 670
 Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr Lys Ile Trp Trp Val His
 25 675 680 685
 Thr Val Phe Thr Lys Lys Glu Glu Lys Lys Glu Trp Arg Lys Thr Leu
 690 695 700
 Glu Pro Trp Lys Leu Tyr Ala Thr Val Gly Leu Leu Val Gly Met Asp
 30 705 710 715 720
 Val Leu Thr Leu Ala Ile Trp Gln Ile Val Asp Pro Leu His Arg Thr
 35 725 730 735
 Ile Glu Thr Phe Ala Lys Glu Glu Pro Lys Glu Asp Ile Asp Val Ser
 740 745 750
 Ile Leu Pro Gln Leu Glu His Cys Ser Ser Lys Lys Met Asn Thr Trp
 40 755 760 765
 Leu Gly Ile Phe Tyr Gly Tyr Lys Gly Leu Leu Leu Leu Gly Ile

	770	775	780	
	Phe Leu Ala Tyr Glu Thr Lys Ser Val Ser Thr Glu Lys Ile Asn Asp			
	785	790	795	800
5	His Arg Ala Val Gly Met Ala Ile Tyr Asn Val Ala Val Leu Cys Leu			
		805	810	815
	Ile Thr Ala Pro Val Thr Met Ile Leu Ser Ser Gln Gln Asp Ala Ala			
10		820	825	830
	Phe Ala Phe Ala Ser Leu Ala Ile Val Phe Ser Ser Tyr Ile Thr Leu			
		835	840	845
15	Val Val Leu Phe Val Pro Lys Met Arg Arg Leu Ile Thr Arg Gly Glu			
		850	855	860
	Trp Gln Ser Glu Thr Gln Asp Thr Met Lys Thr Gly Ser Ser Thr Asn			
	865	870	875	880
20	Asn Asn Glu Glu Glu Lys Ser Arg Leu Leu Glu Lys Glu Asn Arg Glu			
		885	890	895
	Leu Glu Lys Ile Ile Ala Glu Lys Glu Glu Arg Val Ser Glu Leu Arg			
25		900	905	910
	His Gln Leu Gln Ser Arg Gln Gln Leu Arg Ser Arg Arg His Pro Pro			
		915	920	925
30	Thr Pro Pro Asp Pro Ser Gly Gly Leu Pro Arg Gly Pro Ser Glu Pro			
		930	935	940
	Pro Asp Arg Leu Ser Cys Asp Gly Ser Arg Val His Leu Leu Tyr Lys			
	945	950	955	960

35

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 2538 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Rattus norvegicus

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..2532

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Kaupmann, K

Huggel, K

Heid, J

Flor, P

Bischoff, M

Mickel, S

McMaster, G

Angst, C

Bittiger, H

Froestl, W

(B) TITLE: Expression cloning of GABA-B receptors
uncovers similarity to metabotropic glutamate
receptors

(C) JOURNAL: Nature

(D) VOLUME: 386

(F) PAGES: 239-246

(G) DATE: 20 March-1997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

ATG GGC CCG GGG GGA CCC TGT ACC CCA GTG GGG TGG CCG CTG CCT CTT 48
Met Gly Pro Gly Gly Pro Cys Thr Pro Val Gly Trp Pro Leu Pro Leu
1 5 10 15

CTG CTG GTG ATG GCG GCT GGG GTG GCT CCG GTG TGG GCC TCT CAC TCC 96
Leu Leu Val Met Ala Ala Gly Val Ala Pro Val Trp Ala Ser His Ser
20 25 30

	CCT CAT CTC CCG CGG CCT CAC CCG AGG GTC CCC CCG CAC CCC TCC TCA	144
	Pro His Leu Pro Arg Pro His Pro Arg Val Pro Pro His Pro Ser Ser	
	35 40 45	
5	GAA CGG CGT GCA GTA TAC ATC GGG GCG CTG TTT CCC ATG AGC GGG GGC	192
	Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe Pro Met Ser Gly Gly	
	50 55 60	
10	TGG CCG GGG GGC CAG GCC TGC CAG CCC GCG GTG GAG ATG GCG CTG GAG	240
	Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val Glu Met Ala Leu Glu	
	65 70 75 80	
15	GAC GTT AAC AGC CGC AGA GAC ATC CTG CCG GAC TAC GAG CTC AAG CTT	288
	Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp Tyr Glu Leu Lys Leu	
	85 90 95	
20	ATC CAC CAC GAC AGC AAG TGT GAC CCA GGG CAA GCC ACC AAG TAC TTG	336
	Ile His His Asp Ser Lys Cys Asp Pro Gly Gln Ala Thr Lys Tyr Leu	
	100 105 110	
25	TAC GAA CTA CTC TAC AAT GAC CCC ATC AAG ATC ATT CTC ATG CCT GGC	384
	Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile Ile Leu Met Pro Gly	
	115 120 125	
30	TGT AGT TCT GTC TCC ACA CTT GTA GCT GAG GCT GCC CGG ATG TGG AAC	432
	Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala Ala Arg Met Trp Asn	
	130 135 140	
35	CTT ATT GTG CTC TCA TAT GGC TCC AGT TCA CCA GCC TTG TCA AAC CGA	480
	Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro Ala Leu Ser Asn Arg	
	145 150 155 160	
40	CAG CGG TTT CCC ACG TTC TTC CGG ACG CAT CCA TCC GCC ACA CTC CAC	528
	Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro Ser Ala Thr Leu His	
	165 170 175	
45	AAT CCC ACC CGG GTG AAA CTC TTC GAA AAG TGG GGC TGG AAG AAG ATC	576
	Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp Gly Trp Lys Lys Ile	
	180 185 190	
50	GCT ACC ATC CAA CAG ACC ACC GAG GTC TTC ACC TCA ACG CTG GAT GAC	624
	Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr Ser Thr Leu Asp Asp	
	195 200 205	

	CTG GAG GAG CGA GTG AAA GAG GCT GGG ATC GAG ATC ACT TTC CGA CAG	672
	Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu Ile Thr Phe Arg Gln	
	210 215 220	
5	AGT TTC TTC TCG GAT CCA GCT GTG CCT GTT AAA AAC CTG AAG CGT CAA	720
	Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys Asn Leu Lys Arg Gln	
	225 230 235 240	
10	GAT GCT CGA ATC ATC GTG GGA CTT TTC TAT GAG ACG GAA GCC CGG AAA	768
	Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu Thr Glu Ala Arg Lys	
	245 250 255	
	GTT TTT TGT GAG GTC TAT AAG GAA AGG CTC TTT GGG AAG AAG TAC GTC	816
15	Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe Gly Lys Lys Tyr Val	
	260 265 270	
	TGG TTC CTC ATC GGG TGG TAT GCT GAC AAC TGG TTC AAG ACC TAT GAC	864
	Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp Phe Lys Thr Tyr Asp	
20	275 280 285	
	CCG TCA ATC AAT TGT ACA GTG GAA GAA ATG ACC GAG GCG GTG GAG GGC	912
	Pro Ser Ile Asn Cys Thr Val Glu Glu Met Thr Glu Ala Val Glu Gly	
	290 295 300	
25	CAC ATC ACC ACG GAG ATT GTC ATG CTG AAC CCT GCC AAC ACC CGA AGC	960
	His Ile Thr Thr Glu Ile Val Met Leu Asn Pro Ala Asn Thr Arg Ser	
	305 310 315 320	
30	ATT TCC AAC ATG ACG TCA CAG GAA TTT GTG GAG AAA CTA ACC AAG CGG	1008
	Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu Lys Leu Thr Lys Arg	
	325 330 335	
	CTG AAA AGA CAC CCC GAG GAG ACT GGA GGC TTC CAG GAG GCA CCA CTG	1056
35	Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe Gln Glu Ala Pro Leu	
	340 345 350	
	GCC TAT GAT GCT ATC TGG GCC TTG GCT TTG GCC TTG AAC AAG ACG TCT	1104
	Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala Leu Asn Lys Thr Ser	
40	355 360 365	
	GGA GGA GGT GGT CGT TCC GGC GTG CGC CTG GAG GAC TTT AAC TAC AAC	1152
	Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu Asp Phe Asn Tyr Asn	

	370	375	380	
	AAC CAG ACC ATT ACA GAC CAG ATC TAC CGG GCC ATG AAC TCC TCC TCC			1200
	Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala Met Asn Ser Ser Ser			
5	385	390	395	400
	TTT GAG GGC GTT TCT GGC CAT GTG GTC TTT GAT GCC AGC GGC TCC CGG			1248
	Phe Glu Gly Val Ser Gly His Val Val Phe Asp Ala Ser Gly Ser Arg			
	405	410	415	
10	ATG GCA TGG ACA CTT ATC GAG CAG CTA CAG GGC GGC AGC TAC AAG AAG			1296
	Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly Gly Ser Tyr Lys Lys			
	420	425	430	
15	ATC GGC TAC TAC GAC AGC ACC AAG GAT GAT CTT TCC TGG TCC AAA ACG			1344
	Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu Ser Trp Ser Lys Thr			
	435	440	445	
	GAC AAG TGG ATT GGA GGG TCT CCC CCA GCT GAC CAG ACC TTG GTC ATC			1392
20	Asp Lys Trp Ile Gly Gly Ser Pro Pro Ala Asp Gln Thr Leu Val Ile			
	450	455	460	
	AAG ACA TTC CGT TTC CTG TCT CAG AAA CTC TTT ATC TCC GTC TCA GTT			1440
	Lys Thr Phe Arg Phe Leu Ser Gln Lys Leu Phe Ile Ser Val Ser Val			
25	465	470	475	480
	CTC TCC AGC CTG GGC ATT GTT CTT GCT GTT GTC TGT CTG TCC TTT AAC			1488
	Leu Ser Ser Leu Gly Ile Val Leu Ala Val Val Cys Leu Ser Phe Asn			
	485	490	495	
30	ATC TAC AAC TCC CAC GTT CGT TAT ATC CAG AAC TCC CAG CCC AAC CTG			1536
	Ile Tyr Asn Ser His Val Arg Tyr Ile Gln Asn Ser Gln Pro Asn Leu			
	500	505	510	
35	AAC AAT CTG ACT GCT GTG GGC TGC TCA CTG GCA CTG GCT GCT GTC TTC			1584
	Asn Asn Leu Thr Ala Val Gly Cys Ser Leu Ala Leu Ala Ala Val Phe			
	515	520	525	
	CCT CTC GGG CTG GAT GGT TAC CAC ATA GGG AGA AGC CAG TTC CCG TTT			1632
40	Pro Leu Gly Leu Asp Gly Tyr His Ile Gly Arg Ser Gln Phe Pro Phe			
	530	535	540	
	GTC TGC CAG GCC CGC CTT TGG CTC TTG GGC TTG GGC TTT AGT CTG GGC			1680

SUBSTITUTE SHEET (RULE 26)

	TCT CTG GCC ATC GTG TTC TCT TCC TAC ATC ACT CTG GTT GTG CTC TTT	2208
	Ser Leu Ala Ile Val Phe Ser Ser Tyr Ile Thr Leu Val Val Leu Phe	
	725 730 735	
5	GTG CCC AAG ATG CGC AGG CTG ATC ACC CGA GGG GAA TGG CAG TCT GAA	2256
	Val Pro Lys Met Arg Arg Leu Ile Thr Arg Gly Glu Trp Gln Ser Glu	
	740 745 750	
	ACG CAG GAC ACC ATG AAA ACA GGA TCA TCC ACC AAC AAC AAC GAG GAA	2304
10	Thr Gln Asp Thr Met Lys Thr Gly Ser Ser Thr Asn Asn Asn Glu Glu	
	755 760 765	
	GAG AAG TCC CGA CTG TTG GAG AAG GAA AAC CGA GAA CTG GAA AAG ATC	2352
	Glu Lys Ser Arg Leu Leu Glu Lys Glu Asn Arg Glu Leu Glu Lys Ile	
15	770 775 780	
	ATC GCT GAG AAA GAG GAG CGC GTC TCT GAA CTG CGC CAT CAG CTC CAG	2400
	Ile Ala Glu Lys Glu Glu Arg Val Ser Glu Leu Arg His Gln Leu Gln	
	785 790 795 800	
20	TCT CGG CAG CAA CTC CGC TCA CGG CGC CAC CCC CCA ACA CCC CCA GAT	2448
	Ser Arg Gln Gln Leu Arg Ser Arg Arg His Pro Pro Thr Pro Pro Asp	
	805 810 815	
25	CCC TCT GGG GGC CTT CCC AGG GGA CCC TCT GAG CCC CCT GAC CGG CTT	2496
	Pro Ser Gly Gly Leu Pro Arg Gly Pro Ser Glu Pro Pro Asp Arg Leu	
	820 825 830	
	AGC TGT GAT GGG AGT CGA GTA CAT TTG CTT TAC AAG TGA	2535
30	Ser Cys Asp Gly Ser Arg Val His Leu Leu Tyr Lys *	
	835 840	

(2) INFORMATION FOR SEQ ID NO: 47:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 844 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

Met Gly Pro Gly Gly Pro Cys Thr Pro Val Gly Trp Pro Leu Pro Leu
 1 5 10 15

5 Leu Leu Val Met Ala Ala Gly Val Ala Pro Val Trp Ala Ser His Ser
 20 25 30

Pro His Leu Pro Arg Pro His Pro Arg Val Pro Pro His Pro Ser Ser
 35 40 45

10 Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe Pro Met Ser Gly Gly
 50 55 60

Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val Glu Met Ala Leu Glu
 15 65 70 75 80

Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp Tyr Glu Leu Lys Leu
 85 90 95

20 Ile His His Asp Ser Lys Cys Asp Pro Gly Gln Ala Thr Lys Tyr Leu
 100 105 110

Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile Ile Leu Met Pro Gly
 115 120 125

25 Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala Ala Arg Met Trp Asn
 130 135 140

Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro Ala Leu Ser Asn Arg
 30 145 150 155 160

Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro Ser Ala Thr Leu His
 165 170 175

35 Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp Gly Trp Lys Lys Ile
 180 185 190

Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr Ser Thr Leu Asp Asp
 195 200 205

40 Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu Ile Thr Phe Arg Gln
 210 215 220

Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys Asn Leu Lys Arg Gln
 225 230 235 240

Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu Thr Glu Ala Arg Lys
 5 245 250 255

Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe Gly Lys Lys Tyr Val
 260 265 270

10 Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp Phe Lys Thr Tyr Asp
 275 280 285

Pro Ser Ile Asn Cys Thr Val Glu Glu Met Thr Glu Ala Val Glu Gly
 290 295 300

15 His Ile Thr Thr Glu Ile Val Met Leu Asn Pro Ala Asn Thr Arg Ser
 305 310 315 320

Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu Lys Leu Thr Lys Arg
 20 325 330 335

Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe Gln Glu Ala Pro Leu
 340 345 350

25 Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala Leu Asn Lys Thr Ser
 355 360 365

Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu Asp Phe Asn Tyr Asn
 370 375 380

30 Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala Met Asn Ser Ser Ser
 385 390 395 400

Phe Glu Gly Val Ser Gly His Val Val Phe Asp Ala Ser Gly Ser Arg
 35 405 410 415

Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly Gly Ser Tyr Lys Lys
 420 425 430

40 Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu Ser Trp Ser Lys Thr
 435 440 445

Asp Lys Trp Ile Gly Gly Ser Pro Pro Ala Asp Gln Thr Leu Val Ile

450 455 460
 Lys Thr Phe Arg Phe Leu Ser Gln Lys Leu Phe Ile Ser Val Ser Val
 465 470 475 480
 5
 Leu Ser Ser Leu Gly Ile Val Leu Ala Val Val Cys Leu Ser Phe Asn
 485 490 495
 Ile Tyr Asn Ser His Val Arg Tyr Ile Gln Asn Ser Gln Pro Asn Leu
 10 500 505 510
 Asn Asn Leu Thr Ala Val Gly Cys Ser Leu Ala Leu Ala Ala Val Phe
 515 520 525
 15 Pro Leu Gly Leu Asp Gly Tyr His Ile Gly Arg Ser Gln Phe Pro Phe
 530 535 540
 Val Cys Gln Ala Arg Leu Trp Leu Leu Gly Leu Gly Phe Ser Leu Gly
 545 550 555 560
 20 Tyr Gly Ser Met Phe Thr Lys Ile Trp Trp Val His Thr Val Phe Thr
 565 570 575
 Lys Lys Glu Glu Lys Lys Glu Trp Arg Lys Thr Leu Glu Pro Trp Lys
 25 580 585 590
 Leu Tyr Ala Thr Val Gly Leu Leu Val Gly Met Asp Val Leu Thr Leu
 595 600 605
 30 Ala Ile Trp Gln Ile Val Asp Pro Leu His Arg Thr Ile Glu Thr Phe
 610 615 620
 Ala Lys Glu Glu Pro Lys Glu Asp Ile Asp Val Ser Ile Leu Pro Gln
 625 630 635 640
 35 Leu Glu His Cys Ser Ser Lys Lys Met Asn Thr Trp Leu Gly Ile Phe
 645 650 655
 Tyr Gly Tyr Lys Gly Leu Leu Leu Leu Leu Gly Ile Phe Leu Ala Tyr
 40 660 665 670
 Glu Thr Lys Ser Val Ser Thr Glu Lys Ile Asn Asp His Arg Ala Val
 675 680 685

Gly Met Ala Ile Tyr Asn Val Ala Val Leu Cys Leu Ile Thr Ala Pro
 690 695 700
 5 Val Thr Met Ile Leu Ser Ser Gln Gln Asp Ala Ala Phe Ala Phe Ala
 705 710 715 720
 Ser Leu Ala Ile Val Phe Ser Ser Tyr Ile Thr Leu Val Val Leu Phe
 725 730 735
 10 Val Pro Lys Met Arg Arg Leu Ile Thr Arg Gly Glu Trp Gln Ser Glu
 740 745 750
 Thr Gln Asp Thr Met Lys Thr Gly Ser Ser Thr Asn Asn Asn Glu Glu
 15 755 760 765
 Glu Lys Ser Arg Leu Leu Glu Lys Glu Asn Arg Glu Leu Glu Lys Ile
 770 775 780
 20 Ile Ala Glu Lys Glu Glu Arg Val Ser Glu Leu Arg His Gln Leu Gln
 785 790 795 800
 Ser Arg Gln Gln Leu Arg Ser Arg Arg His Pro Pro Thr Pro Pro Asp
 805 810 815
 25 Pro Ser Gly Gly Leu Pro Arg Gly Pro Ser Glu Pro Pro Asp Arg Leu
 820 825 830
 Ser Cys Asp Gly Ser Arg Val His Leu Leu Tyr Lys
 30 835 840

(2) INFORMATION FOR SEQ ID NO: 48:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2886 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 40
 (ii) MOLECULE TYPE: cDNA to mRNA
 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

5 (A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..2886

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

	ATG TTG CTG CTG CTG CTA CTG GCG CCA CTC TTC CTC CGC CCC CCG GGC	48
	Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly	
15	1 5 10 15	
	GCG GGC GGG GCG CAG ACC CCC AAC GCC ACC TCA GAA GGT TGC CAG ATC	96
	Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile	
	20 25 30	
20	ATA CAC CCG CCC TGG GAA GGG GGC ATC AGG TAC CGG GGC CTG ACT CGG	144
	Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg	
	35 40 45	
25	GAC CAG GTG AAG GCT ATC AAC TTC CTG CCA GTG GAC TAT GAG ATT GAG	192
	Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu	
	50 55 60	
	TAT GTG TGC CGG GGG GAG CGC GAG GTG GTG GGG CCC AAG GTC CGC AAG	240
30	Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys	
	65 70 75 80	
	TGC CTG GCC AAC GGC TCC TGG ACA GAT ATG GAC ACA CCC AGC CGC TGT	288
	Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys	
35	85 90 95	
	GTC CGA ATC TGC TCC AAG TCT TAT TTG ACC CTG GAA AAT GGG AAG GTT	336
	Val Arg Ile Cys Ser Lys Ser Tyr Leu Thr Leu Glu Asn Gly Lys Val	
	100 105 110	
40	TTC CTG ACG GGT GGG GAC CTC CCA GCT CTG GAC GGA GCC CGG GTG GAT	384
	Phe Leu Thr Gly Gly Asp Leu Pro Ala Leu Asp Gly Ala Arg Val Asp	
	115 120 125	

	TTC CGG TGT GAC CCC GAC TTC CAT CTG GTG GGC AGC TCC CGG AGC ATC	432
	Phe Arg Cys Asp Pro Asp Phe His Leu Val Gly Ser Ser Arg Ser Ile	
	130 135 140	
5	TGT AGT CAG GGC CAG TGG AGC ACC CCC AAG CCC CAC TGC CAG GTG AAT	480
	Cys Ser Gln Gly Gln Trp Ser Thr Pro Lys Pro His Cys Gln Val Asn	
	145 150 155 160	
10	CGA ACG CCA CAC TCA GAA CGG CGC GCA GTG TAC ATC GGG GCA CTG TTT	528
	Arg Thr Pro His Ser Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe	
	165 170 175	
	CCC ATG AGC GGG GGC TGG CCA GGG GGC CAG GCC TGC CAG CCC GCG GTG	576
15	Pro Met Ser Gly Gly Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val	
	180 185 190	
	GAG ATG GCG CTG GAG GAC GTG AAT AGC CGC AGG GAC ATC CTG CCG GAC	624
	Glu Met Ala Leu Glu Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp	
20	195 200 205	
	TAT GAG CTC AAG CTC ATC CAC CAC GAC AGC AAG TGT GAT CCA GGC CAA	672
	Tyr Glu Leu Lys Leu Ile His His Asp Ser Lys Cys Asp Pro Gly Gln	
	210 215 220	
25	GCC ACC AAG TAC CTA TAT GAG CTG CTC TAC AAC GAC CCT ATC AAG ATC	720
	Ala Thr Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile	
	225 230 235 240	
30	ATC CTT ATG CCT GGC TGC AGC TCT GTC TCC ACG CTG GTG GCT GAG GCT	768
	Ile Leu Met Pro Gly Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala	
	245 250 255	
	GCT AGG ATG TGG AAC CTC ATT GTG CTT TCC TAT GGC TCC AGC TCA CCA	816
35	Ala Arg Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro	
	260 265 270	
	GCC CTG TCA AAC CGG CAG CGT TTC CCC ACT TTC TTC CGA ACG CAC CCA	864
	Ala Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro	
40	275 280 285	
	TCA GCC ACA CTC CAC AAC CCT ACC CGC GTG AAA CTC TTT GAA AAG TGG	912
	Ser Ala Thr Leu His Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp	

	290	295	300	
	GGC TGG AAG AAG ATT GCT ACC ATC CAG CAG ACC ACT GAG GTC TTC ACT			960
	Gly Trp Lys Lys Ile Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr			
5	305	310	315	320
	TCG ACT CTG GAC GAC CTG GAG GAA CGA GTG AAG GAG GCT GGA ATT GAG			1008
	Ser Thr Leu Asp Asp Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu			
	325	330	335	
10	ATT ACT TTC CGC CAG AGT TTC TTC TCA GAT CCA GCT GTG CCC GTC AAA			1056
	Ile Thr Phe Arg Gln Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys			
	340	345	350	
15	AAC CTG AAG CGC CAG GAT GCC CGA ATC ATC GTG GGA CTT TTC TAT GAG			1104
	Asn Leu Lys Arg Gln Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu			
	355	360	365	
	ACT GAA GCC CGG AAA GTT TTT TGT GAG GTG TAC AAG GAG CGT CTC TTT			1152
20	Thr Glu Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe			
	370	375	380	
	GGG AAG AAG TAC GTC TGG TTC CTC ATT GGG TGG TAT GCT GAC AAT TGG			1200
	Gly Lys Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp			
25	385	390	395	400
	TTC AAG ATC TAC GAC CCT TCT ATC AAC TGC ACA GTG GAT GAG ATG ACT			1248
	Phe Lys Ile Tyr Asp Pro Ser Ile Asn Cys Thr Val Asp Glu Met Thr			
	405	410	415	
30	GAG GCG GTG GAG GGC CAC ATC ACA ACT GAG ATT GTC ATG CTG AAT CCT			1296
	Glu Ala Val Glu Gly His Ile Thr Thr Glu Ile Val Met Leu Asn Pro			
	420	425	430	
35	GCC AAT ACC CGC AGC ATT TCC AAC ATG ACA TCC CAG GAA TTT GTG GAG			1344
	Ala Asn Thr Arg Ser Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu			
	435	440	445	
	AAA CTA ACC AAG CGA CTG AAA AGA CAC CCT GAG GAG ACA GGA GGC TTC			1392
40	Lys Leu Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe			
	450	455	460	
	CAG GAG GCA CCG CTG GCC TAT GAT GCC ATC TGG GCC TTG GCA CTG GCC			1440

	Gln	Glu	Ala	Pro	Leu	Ala	Tyr	Asp	Ala	Ile	Trp	Ala	Leu	Ala	Leu	Ala	
	465					470					475					480	
	CTG	AAC	AAG	ACA	TCT	GGA	GGA	GGC	GGC	CGT	TCT	GGT	GTG	CGC	CTG	GAG	1488
5	Leu	Asn	Lys	Thr	Ser	Gly	Gly	Gly	Gly	Arg	Ser	Gly	Val	Arg	Leu	Glu	
					485					490					495		
	GAC	TTC	AAC	TAC	AAC	AAC	CAG	ACC	ATT	ACC	GAC	CAA	ATC	TAC	CGG	GCA	1536
10	Asp	Phe	Asn	Tyr	Asn	Asn	Gln	Thr	Ile	Thr	Asp	Gln	Ile	Tyr	Arg	Ala	
				500					505					510			
	ATG	AAC	TCT	TCG	TCC	TTT	GAG	GGT	GTC	TCT	GGC	CAT	GTG	GTG	TTT	GAT	1584
	Met	Asn	Ser	Ser	Ser	Phe	Glu	Gly	Val	Ser	Gly	His	Val	Val	Phe	Asp	
			515					520					525				
15																	
	GCC	AGC	GGC	TCT	CGG	ATG	GCA	TGG	ACG	CTT	ATC	GAG	CAG	CTT	CAG	GGT	1632
	Ala	Ser	Gly	Ser	Arg	Met	Ala	Trp	Thr	Leu	Ile	Glu	Gln	Leu	Gln	Gly	
			530				535					540					
20																	
	GGC	AGC	TAC	AAG	AAG	ATT	GGC	TAC	TAT	GAC	AGC	ACC	AAG	GAT	GAT	CTT	1680
	Gly	Ser	Tyr	Lys	Lys	Ile	Gly	Tyr	Tyr	Asp	Ser	Thr	Lys	Asp	Asp	Leu	
	545					550					555					560	
25																	
	TCC	TGG	TCC	AAA	ACA	GAT	AAA	TGG	ATT	GGA	GGG	TCC	CCC	CCA	GCT	GAC	1728
	Ser	Trp	Ser	Lys	Thr	Asp	Lys	Trp	Ile	Gly	Gly	Ser	Pro	Pro	Ala	Asp	
					565					570					575		
	CAG	ACC	CTG	GTC	ATC	AAG	ACA	TTC	CGC	TTC	CTG	TCA	CAG	AAA	CTC	TTT	1776
30	Gln	Thr	Leu	Val	Ile	Lys	Thr	Phe	Arg	Phe	Leu	Ser	Gln	Lys	Leu	Phe	
				580					585					590			
	ATC	TCC	GTC	TCA	GTT	CTC	TCC	AGC	CTG	GGC	ATT	GTC	CTA	GCT	GTT	GTC	1824
	Ile	Ser	Val	Ser	Val	Leu	Ser	Ser	Leu	Gly	Ile	Val	Leu	Ala	Val	Val	
			595					600					605				
35																	
	TGT	CTG	TCC	TTT	AAC	ATC	TAC	AAC	TCA	CAT	GTC	CGT	TAT	ATC	CAG	AAC	1872
	Cys	Leu	Ser	Phe	Asn	Ile	Tyr	Asn	Ser	His	Val	Arg	Tyr	Ile	Gln	Asn	
		610					615					620					
40																	
	TCA	CAG	CCC	AAC	CTG	AAC	AAC	CTG	ACT	GCT	GTG	GGC	TGC	TCA	CTG	GCT	1920
	Ser	Gln	Pro	Asn	Leu	Asn	Asn	Leu	Thr	Ala	Val	Gly	Cys	Ser	Leu	Ala	
	625					630					635				640		

	TTA GCT GCT GTC TTC CCC CTG GGG CTC GAT GGT TAC CAC ATT GGG AGG	1968
	Leu Ala Ala Val Phe Pro Leu Gly Leu Asp Gly Tyr His Ile Gly Arg	
	645 650 655	
5	AAC CAG TTT CCT TTC GTC TGC CAG GCC CGC CTC TGG CTC CTG GGC CTG	2016
	Asn Gln Phe Pro Phe Val Cys Gln Ala Arg Leu Trp Leu Leu Gly Leu	
	660 665 670	
	GGC TTT AGT CTG GGC TAC GGT TCC ATG TTC ACC AAG ATT TGG TGG GTC	2064
10	Gly Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr Lys Ile Trp Trp Val	
	675 680 685	
	CAC ACG GTC TTC ACA AAG AAG GAA GAA AAG AAG GAG TGG AGG AAG ACT	2112
	His Thr Val Phe Thr Lys Lys Glu Glu Lys Lys Glu Trp Arg Lys Thr	
15	690 695 700	
	CTG GAA CCC TGG AAG CTG TAT GCC ACA GTG GGC CTG CTG GTG GGC ATG	2160
	Leu Glu Pro Trp Lys Leu Tyr Ala Thr Val Gly Leu Leu Val Gly Met	
	705 710 715 720	
20	GAT GTC CTC ACT CTC GCC ATC TGG CAG ATC GTG GAC CCT CTG CAC CGG	2208
	Asp Val Leu Thr Leu Ala Ile Trp Gln Ile Val Asp Pro Leu His Arg	
	725 730 735	
	ACC ATT GAG ACA TTT GCC AAG GAG GAA CCT AAG GAA GAT ATT GAC GTC	2256
25	Thr Ile Glu Thr Phe Ala Lys Glu Glu Pro Lys Glu Asp Ile Asp Val	
	740 745 750	
	TCT ATT CTG CCC CAG CTG GAG CAT TGC AGC TCC AGG AAG ATG AAT ACA	2304
30	Ser Ile Leu Pro Gln Leu Glu His Cys Ser Ser Arg Lys Met Asn Thr	
	755 760 765	
	TGG CTT GGC ATT TTC TAT GGT TAC AAG GGG CTG CTG CTG CTG CTG GGA	2352
	Trp Leu Gly Ile Phe Tyr Gly Tyr Lys Gly Leu Leu Leu Leu Leu Gly	
35	770 775 780	
	ATC TTC CTT GCT TAT GAG ACC AAG AGT GTG TCC ACT GAG AAG ATC AAT	2400
	Ile Phe Leu Ala Tyr Glu Thr Lys Ser Val Ser Thr Glu Lys Ile Asn	
	785 790 795 800	
40	GAT CAC CGG GCT GTG GGC ATG GCT ATC TAC AAT GTG GCA GTC CTG TGC	2448
	Asp His Arg Ala Val Gly Met Ala Ile Tyr Asn Val Ala Val Leu Cys	
	805 810 815	

	CTC ATC ACT GCT CCT GTC ACC ATG ATT CTG TCC AGC CAG CAG GAT GCA	2496
	Leu Ile Thr Ala Pro Val Thr Met Ile Leu Ser Ser Gln Gln Asp Ala	
	820 825 830	
5	GCC TTT GCC TTT GCC TCT CTT GCC ATA GTT TTC TCC TCC TAT ATC ACT	2544
	Ala Phe Ala Phe Ala Ser Leu Ala Ile Val Phe Ser Ser Tyr Ile Thr	
	835 840 845	
10	CTT GTT GTG CTC TTT GTG CCC AAG ATG CGC AGG CTG ATC ACC CGA GGG	2592
	Leu Val Val Leu Phe Val Pro Lys Met Arg Arg Leu Ile Thr Arg Gly	
	850 855 860	
	GAA TGG CAG TCG GAG GCG CAG GAC ACC ATG AAG ACA GGG TCA TCG ACC	2640
15	Glu Trp Gln Ser Glu Ala Gln Asp Thr Met Lys Thr Gly Ser Ser Thr	
	865 870 875 880	
	AAC AAC AAC GAG GAG GAG AAG TCC CGG CTG TTG GAG AAG GAG AAC CGT	2688
	Asn Asn Asn Glu Glu Glu Lys Ser Arg Leu Leu Glu Lys Glu Asn Arg	
20	885 890 895	
	GAA CTG GAA AAG ATC ATT GCT GAG AAA GAG GAG CGT GTC TCT GAA CTG	2736
	Glu Leu Glu Lys Ile Ile Ala Glu Lys Glu Glu Arg Val Ser Glu Leu	
	900 905 910	
25	CGC CAT CAA CTC CAG TCT CGG CAG CAG CTC CGC TCC CGG CGC CAC CCA	2784
	Arg His Gln Leu Gln Ser Arg Gln Gln Leu Arg Ser Arg Arg His Pro	
	915 920 925	
30	CCG ACA CCC CCA GAA CCC TCT GGG GGC CTG CCC AGG GGA CCC CCT GAG	2832
	Pro Thr Pro Pro Glu Pro Ser Gly Gly Leu Pro Arg Gly Pro Pro Glu	
	930 935 940	
	CCC CCC GAC CGG CTT AGC TGT GAT GGG AGT CGA GTG CAT TTG CTT TAT	2880
35	Pro Pro Asp Arg Leu Ser Cys Asp Gly Ser Arg Val His Leu Leu Tyr	
	945 950 955 960	
	AAG TGA	2886
	Lys *	

40

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 961 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

10

Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly
 1 5 10 15

15

Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile
 20 25 30

Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg
 35 40 45

20

Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu
 50 55 60

Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys
 65 70 75 80

25

Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys
 85 90 95

30

Val Arg Ile Cys Ser Lys Ser Tyr Leu Thr Leu Glu Asn Gly Lys Val
 100 105 110

Phe Leu Thr Gly Gly Asp Leu Pro Ala Leu Asp Gly Ala Arg Val Asp
 115 120 125

35

Phe Arg Cys Asp Pro Asp Phe His Leu Val Gly Ser Ser Arg Ser Ile
 130 135 140

Cys Ser Gln Gly Gln Trp Ser Thr Pro Lys Pro His Cys Gln Val Asn
 145 150 155 160

40

Arg Thr Pro His Ser Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe
 165 170 175

Pro Met Ser Gly Gly Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val
 180 185 190

5 Glu Met Ala Leu Glu Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp
 195 200 205

Tyr Glu Leu Lys Leu Ile His His Asp Ser Lys Cys Asp Pro Gly Gln
 210 215 220

10 Ala Thr Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile
 225 230 235 240

Ile Leu Met Pro Gly Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala
 245 250 255

15 Ala Arg Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro
 260 265 270

20 Ala Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro
 275 280 285

Ser Ala Thr Leu His Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp
 290 295 300

25 Gly Trp Lys Lys Ile Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr
 305 310 315 320

Ser Thr Leu Asp Asp Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu
 325 330 335

30 Ile Thr Phe Arg Gln Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys
 340 345 350

Asn Leu Lys Arg Gln Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu
 355 360 365

35 Thr Glu Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe
 370 375 380

40 Gly Lys Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp
 385 390 395 400

Phe Lys Ile Tyr Asp Pro Ser Ile Asn Cys Thr Val Asp Glu Met Thr

	405	410	415
	Glu Ala Val Glu Gly His Ile Thr Thr Glu Ile Val Met Leu Asn Pro		
	420	425	430
5	Ala Asn Thr Arg Ser Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu		
	435	440	445
	Lys Leu Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe		
10	450	455	460
	Gln Glu Ala Pro Leu Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala		
	465	470	475 480
15	Leu Asn Lys Thr Ser Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu		
	485	490	495
	Asp Phe Asn Tyr Asn Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala		
	500	505	510
20	Met Asn Ser Ser Ser Phe Glu Gly Val Ser Gly His Val Val Phe Asp		
	515	520	525
	Ala Ser Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly		
25	530	535	540
	Gly Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu		
	545	550	555 560
30	Ser Trp Ser Lys Thr Asp Lys Trp Ile Gly Gly Ser Pro Pro Ala Asp		
	565	570	575
	Gln Thr Leu Val Ile Lys Thr Phe Arg Phe Leu Ser Gln Lys Leu Phe		
	580	585	590
35	Ile Ser Val Ser Val Leu Ser Ser Leu Gly Ile Val Leu Ala Val Val		
	595	600	605
	Cys Leu Ser Phe Asn Ile Tyr Asn Ser His Val Arg Tyr Ile Gln Asn		
40	610	615	620
	Ser Gln Pro Asn Leu Asn Asn Leu Thr Ala Val Gly Cys Ser Leu Ala		
	625	630	635 640

Leu Ala Ala Val Phe Pro Leu Gly Leu Asp Gly Tyr His Ile Gly Arg
 645 650 655

5 Asn Gln Phe Pro Phe Val Cys Gln Ala Arg Leu Trp Leu Leu Gly Leu
 660 665 670

Gly Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr Lys Ile Trp Trp Val
 675 680 685

10 His Thr Val Phe Thr Lys Lys Glu Glu Lys Lys Glu Trp Arg Lys Thr
 690 695 700

Leu Glu Pro Trp Lys Leu Tyr Ala Thr Val Gly Leu Leu Val Gly Met
 15 705 710 715 720

Asp Val Leu Thr Leu Ala Ile Trp Gln Ile Val Asp Pro Leu His Arg
 725 730 735

20 Thr Ile Glu Thr Phe Ala Lys Glu Glu Pro Lys Glu Asp Ile Asp Val
 740 745 750

Ser Ile Leu Pro Gln Leu Glu His Cys Ser Ser Arg Lys Met Asn Thr
 755 760 765

25 Trp Leu Gly Ile Phe Tyr Gly Tyr Lys Gly Leu Leu Leu Leu Gly
 770 775 780

Ile Phe Leu Ala Tyr Glu Thr Lys Ser Val Ser Thr Glu Lys Ile Asn
 30 785 790 795 800

Asp His Arg Ala Val Gly Met Ala Ile Tyr Asn Val Ala Val Leu Cys
 805 810 815

35 Leu Ile Thr Ala Pro Val Thr Met Ile Leu Ser Ser Gln Gln Asp Ala
 820 825 830

Ala Phe Ala Phe Ala Ser Leu Ala Ile Val Phe Ser Ser Tyr Ile Thr
 835 840 845

40 Leu Val Val Leu Phe Val Pro Lys Met Arg Arg Leu Ile Thr Arg Gly
 850 855 860

Glu Trp Gln Ser Glu Ala Gln Asp Thr Met Lys Thr Gly Ser Ser Thr
 865 870 875 880
 Asn Asn Asn Glu Glu Glu Lys Ser Arg Leu Leu Glu Lys Glu Asn Arg
 5 885 890 895
 Glu Leu Glu Lys Ile Ile Ala Glu Lys Glu Glu Arg Val Ser Glu Leu
 900 905 910
 Arg His Gln Leu Gln Ser Arg Gln Gln Leu Arg Ser Arg Arg His Pro
 10 915 920 925
 Pro Thr Pro Pro Glu Pro Ser Gly Gly Leu Pro Arg Gly Pro Pro Glu
 930 935 940
 Pro Pro Asp Arg Leu Ser Cys Asp Gly Ser Arg Val His Leu Leu Tyr
 15 945 950 955 960
 Lys
 20

(2) INFORMATION FOR SEQ ID NO: 50:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2535 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 30
 (ii) MOLECULE TYPE: cDNA to rRNA
 (iii) HYPOTHETICAL: NO
 35 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
 40 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..2535

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

5	1	5	10	15	48
	ATG GGG CCC GGG GCC CCT TTT GCC CGG GTG GGG TGG CCA CTG CCG CTT				
	Met Gly Pro Gly Ala Pro Phe Ala Arg Val Gly Trp Pro Leu Pro Leu				
10	20	25	30		96
	CTG GTT GTG ATG GCG GCA GGG GTG GCT CCG GTG TGG GCC TCC CAC TCC				
	Leu Val Val Met Ala Ala Gly Val Ala Pro Val Trp Ala Ser His Ser				
15	35	40	45		144
	CCC CAT CTC CCG CGG CCT CAC TCG CGG GTC CCC CCG CAC CCC TCC TCA				
	Pro His Leu Pro Arg Pro His Ser Arg Val Pro Pro His Pro Ser Ser				
20	50	55	60		192
	GAA CGG CGC GCA GTG TAC ATC GGG GCA CTG TTT CCC ATG AGC GGG GGC				
	Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe Pro Met Ser Gly Gly				
25	65	70	75	80	240
	TGG CCA GGG GGC CAG GCC TGC CAG CCC GCG GTG GAG ATG GCG CTG GAG				
	Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val Glu Met Ala Leu Glu				
30	85	90	95		288
	GAC GTG AAT AGC CGC AGG GAC ATC CTG CCG GAC TAT GAG CTC AAG CTC				
	Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp Tyr Glu Leu Lys Leu				
35	100	105	110		336
	ATC CAC CAC GAC AGC AAG TGT GAT CCA GGC CAA GCC ACC AAG TAC CTA				
	Ile His His Asp Ser Lys Cys Asp Pro Gly Gln Ala Thr Lys Tyr Leu				
40	115	120	125		384
	TAT GAG CTG CTC TAC AAC GAC CCT ATC AAG ATC ATC CTT ATG CCT GGC				
	Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile Ile Leu Met Pro Gly				
45	130	135	140		432
	TGC AGC TCT GTC TCC ACG CTG GTG GCT GAG GCT GCT AGG ATG TGG AAC				
	Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala Ala Arg Met Trp Asn				
50	145	150	155	160	480
	CTC ATT GTG CTT TCC TAT GGC TCC AGC TCA CCA GCC CTG TCA AAC CGG				
	Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro Ala Leu Ser Asn Arg				
55					528
	CAG CGT TTC CCC ACT TTC TTC CGA ACG CAC CCA TCA GCC ACA CTC CAC				

	Gln	Arg	Phe	Pro	Thr	Phe	Phe	Arg	Thr	His	Pro	Ser	Ala	Thr	Leu	His	
					165					170					175		
	AAC	CCT	ACC	CGC	GTG	AAA	CTC	TTT	GAA	AAG	TGG	GGC	TGG	AAG	AAG	ATT	576
5	Asn	Pro	Thr	Arg	Val	Lys	Leu	Phe	Glu	Lys	Trp	Gly	Trp	Lys	Lys	Ile	
					180					185					190		
	GCT	ACC	ATC	CAG	CAG	ACC	ACT	GAG	GTC	TTC	ACT	TCG	ACT	CTG	GAC	GAC	624
10	Ala	Thr	Ile	Gln	Gln	Thr	Thr	Glu	Val	Phe	Thr	Ser	Thr	Leu	Asp	Asp	
					195					200					205		
	CTG	GAG	GAA	CGA	GTG	AAG	GAG	GCT	GGA	ATT	GAG	ATT	ACT	TTC	CGC	CAG	672
	Leu	Glu	Glu	Arg	Val	Lys	Glu	Ala	Gly	Ile	Glu	Ile	Thr	Phe	Arg	Gln	
					210					215					220		
15	AGT	TTC	TTC	TCA	GAT	CCA	GCT	GTG	CCC	GTC	AAA	AAC	CTG	AAG	CGC	CAG	720
	Ser	Phe	Phe	Ser	Asp	Pro	Ala	Val	Pro	Val	Lys	Asn	Leu	Lys	Arg	Gln	
					225					230					235		240
20	GAT	GCC	CGA	ATC	ATC	GTG	GGA	CTT	TTC	TAT	GAG	ACT	GAA	GCC	CGG	AAA	768
	Asp	Ala	Arg	Ile	Ile	Val	Gly	Leu	Phe	Tyr	Glu	Thr	Glu	Ala	Arg	Lys	
						245				250					255		
	GTT	TTT	TGT	GAG	GTG	TAC	AAG	GAG	CGT	CTC	TTT	GGG	AAG	AAG	TAC	GTC	816
25	Val	Phe	Cys	Glu	Val	Tyr	Lys	Glu	Arg	Leu	Phe	Gly	Lys	Lys	Tyr	Val	
						260				265					270		
	TGG	TTC	CTC	ATT	GGG	TGG	TAT	GCT	GAC	AAT	TGG	TTC	AAG	ATC	TAC	GAC	864
30	Trp	Phe	Leu	Ile	Gly	Trp	Tyr	Ala	Asp	Asn	Trp	Phe	Lys	Ile	Tyr	Asp	
					275					280					285		
	CCT	TCT	ATC	AAC	TGC	ACA	GTG	GAT	GAG	ATG	ACT	GAG	GCG	GTG	GAG	GGC	912
	Pro	Ser	Ile	Asn	Cys	Thr	Val	Asp	Glu	Met	Thr	Glu	Ala	Val	Glu	Gly	
					290					295					300		
35	CAC	ATC	ACA	ACT	GAG	ATT	GTC	ATG	CTG	AAT	CCT	GCC	AAT	ACC	CGC	AGC	960
	His	Ile	Thr	Thr	Glu	Ile	Val	Met	Leu	Asn	Pro	Ala	Asn	Thr	Arg	Ser	
					305					310					315		320
40	ATT	TCC	AAC	ATG	ACA	TCC	CAG	GAA	TTT	GTG	GAG	AAA	CTA	ACC	AAG	CGA	1008
	Ile	Ser	Asn	Met	Thr	Ser	Gln	Glu	Phe	Val	Glu	Lys	Leu	Thr	Lys	Arg	
						325				330					335		

	CTG AAA AGA CAC CCT GAG GAG ACA GGA GGC TTC CAG GAG GCA CCG CTG	1056
	Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe Gln Glu Ala Pro Leu	
	340 345 350	
5	GCC TAT GAT GCC ATC TGG GCC TTG GCA CTG GCC CTG AAC AAG ACA TCT	1104
	Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala Leu Asn Lys Thr Ser	
	355 360 365	
10	GGA GGA GGC GGC CGT TCT GGT GTG CGC CTG GAG GAC TTC AAC TAC AAC	1152
	Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu Asp Phe Asn Tyr Asn	
	370 375 380	
15	AAC CAG ACC ATT ACC GAC CAA ATC TAC CGG GCA ATG AAC TCT TCG TCC	1200
	Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala Met Asn Ser Ser Ser	
	385 390 395 400	
20	TTT GAG GGT GTC TCT GGC CAT GTG GTG TTT GAT GCC AGC GGC TCT CGG	1248
	Phe Glu Gly Val Ser Gly His Val Val Phe Asp Ala Ser Gly Ser Arg	
	405 410 415	
	ATG GCA TGG ACG CTT ATC GAG CAG CTT CAG GGT GGC AGC TAC AAG AAG	1296
	Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly Gly Ser Tyr Lys Lys	
	420 425 430	
25	ATT GGC TAC TAT GAC AGC ACC AAG GAT GAT CTT TCC TGG TCC AAA ACA	1344
	Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu Ser Trp Ser Lys Thr	
	435 440 445	
30	GAT AAA TGG ATT GGA GGG TCC CCC CCA GCT GAC CAG ACC CTG GTC ATC	1392
	Asp Lys Trp Ile Gly Gly Ser Pro Pro Ala Asp Gln Thr Leu Val Ile	
	450 455 460	
35	AAG ACA TTC CGC TTC CTG TCA CAG AAA CTC TTT ATC TCC GTC TCA GTT	1440
	Lys Thr Phe Arg Phe Leu Ser Gln Lys Leu Phe Ile Ser Val Ser Val	
	465 470 475 480	
40	CTC TCC AGC CTG GGC ATT GTC CTA GCT GTT GTC TGT CTG TCC TTT AAC	1488
	Leu Ser Ser Leu Gly Ile Val Leu Ala Val Val Cys Leu Ser Phe Asn	
	485 490 495	
	ATC TAC AAC TCA CAT GTC CGT TAT ATC CAG AAC TCA CAG CCC AAC CTG	1536
	Ile Tyr Asn Ser His Val Arg Tyr Ile Gln Asn Ser Gln Pro Asn Leu	
	500 505 510	

	AAC AAC CTG ACT GCT GTG GGC TGC TCA CTG GCT TTA GCT GCT GTC TTC	1584
	Asn Asn Leu Thr Ala Val Gly Cys Ser Leu Ala Leu Ala Ala Val Phe	
	515 520 525	
5	CCC CTG GGG CTC GAT GGT TAC CAC ATT GGG AGG AAC CAG TTT CCT TTC	1632
	Pro Leu Gly Leu Asp Gly Tyr His Ile Gly Arg Asn Gln Phe Pro Phe	
	530 535 540	
10	GTC TGC CAG GCC CGC CTC TGG CTC CTG GGC CTG GGC TTT AGT CTG GGC	1680
	Val Cys Gln Ala Arg Leu Trp Leu Leu Gly Leu Gly Phe Ser Leu Gly	
	545 550 555 560	
	TAC GGT TCC ATG TTC ACC AAG ATT TGG TGG GTC CAC ACG GTC TTC ACA	1728
15	Tyr Gly Ser Met Phe Thr Lys Ile Trp Trp Val His Thr Val Phe Thr	
	565 570 575	
	AAG AAG GAA GAA AAG AAG GAG TGG AGG AAG ACT CTG GAA CCC TGG AAG	1776
	Lys Lys Glu Glu Lys Lys Glu Trp Arg Lys Thr Leu Glu Pro Trp Lys	
20	580 585 590	
	CTG TAT GCC ACA GTG GGC CTG CTG GTG GGC ATG GAT GTC CTC ACT CTC	1824
	Leu Tyr Ala Thr Val Gly Leu Leu Val Gly Met Asp Val Leu Thr Leu	
	595 600 605	
25	GCC ATC TGG CAG ATC GTG GAC CCT CTG CAC CGG ACC ATT GAG ACA TTT	1872
	Ala Ile Trp Gln Ile Val Asp Pro Leu His Arg Thr Ile Glu Thr Phe	
	610 615 620	
30	GCC AAG GAG GAA CCT AAG GAA GAT ATT GAC GTC TCT ATT CTG CCC CAG	1920
	Ala Lys Glu Glu Pro Lys Glu Asp Ile Asp Val Ser Ile Leu Pro Gln	
	625 630 635 640	
	CTG GAG CAT TGC AGC TCC AGG AAG ATG AAT ACA TGG CTT GGC ATT TTC	1968
35	Leu Glu His Cys Ser Ser Arg Lys Met Asn Thr Trp Leu Gly Ile Phe	
	645 650 655	
	TAT GGT TAC AAG GGG CTG CTG CTG CTG CTG GGA ATC TTC CTT GCT TAT	2016
	Tyr Gly Tyr Lys Gly Leu Leu Leu Leu Leu Gly Ile Phe Leu Ala Tyr	
40	660 665 670	
	GAG ACC AAG AGT GTG TCC ACT GAG AAG ATC AAT GAT CAC CGG GCT GTG	2064
	Glu Thr Lys Ser Val Ser Thr Glu Lys Ile Asn Asp His Arg Ala Val	

	675	680	685	
	GGC ATG GCT ATC TAC AAT GTG GCA GTC CTG TGC CTC ATC ACT GCT CCT	2112		
	Gly Met Ala Ile Tyr Asn Val Ala Val Leu Cys Leu Ile Thr Ala Pro			
5	690	695	700	
	GTC ACC ATG ATT CTG TCC AGC CAG CAG GAT GCA GCC TTT GCC TTT GCC	2160		
	Val Thr Met Ile Leu Ser Ser Gln Gln Asp Ala Ala Phe Ala Phe Ala			
	705	710	715	720
10				
	TCT CTT GCC ATA GTT TTC TCC TCC TAT ATC ACT CTT GTT GTG CTC TTT	2208		
	Ser Leu Ala Ile Val Phe Ser Ser Tyr Ile Thr Leu Val Val Leu Phe			
	725	730	735	
15				
	GTG CCC AAG ATG CGC AGG CTG ATC ACC CGA GGG GAA TGG CAG TCG GAG	2256		
	Val Pro Lys Met Arg Arg Leu Ile Thr Arg Gly Glu Trp Gln Ser Glu			
	740	745	750	
	GCG CAG GAC ACC ATG AAG ACA GGG TCA TCG ACC AAC AAC AAC GAG GAG	2304		
20	Ala Gln Asp Thr Met Lys Thr Gly Ser Ser Thr Asn Asn Asn Glu Glu			
	755	760	765	
	GAG AAG TCC CGG CTG TTG GAG AAG GAG AAC CGT GAA CTG GAA AAG ATC	2352		
	Glu Lys Ser Arg Leu Leu Glu Lys Glu Asn Arg Glu Leu Glu Lys Ile			
25	770	775	780	
	ATT GCT GAG AAA GAG GAG CGT GTC TCT GAA CTG CGC CAT CAA CTC CAG	2400		
	Ile Ala Glu Lys Glu Glu Arg Val Ser Glu Leu Arg His Gln Leu Gln			
	785	790	795	800
30				
	TCT CGG CAG CAG CTC CGC TCC CGG CGC CAC CCA CCG ACA CCC CCA GAA	2448		
	Ser Arg Gln Gln Leu Arg Ser Arg Arg His Pro Pro Thr Pro Pro Glu			
	805	810	815	
35				
	CCC TCT GGG GGC CTG CCC AGG GGA CCC CCT GAG CCC CCC GAC CGG CTT	2496		
	Pro Ser Gly Gly Leu Pro Arg Gly Pro Pro Glu Pro Pro Asp Arg Leu			
	820	825	830	
	AGC TGT GAT GGG AGT CGA GTG CAT TTG CTT TAT AAG TGA	2535		
40	Ser Cys Asp Gly Ser Arg Val His Leu Leu Tyr Lys *			
	835	840		

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 844 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

Met Gly Pro Gly Ala Pro Phe Ala Arg Val Gly Trp Pro Leu Pro Leu
 1 5 10 15
 Leu Val Val Met Ala Ala Gly Val Ala Pro Val Trp Ala Ser His Ser
 20 25 30
 Pro His Leu Pro Arg Pro His Ser Arg Val Pro Pro His Pro Ser Ser
 35 40 45
 Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe Pro Met Ser Gly Gly
 50 55 60
 Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val Glu Met Ala Leu Glu
 65 70 75 80
 Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp Tyr Glu Leu Lys Leu
 85 90 95
 Ile His His Asp Ser Lys Cys Asp Pro Gly Gln Ala Thr Lys Tyr Leu
 100 105 110
 Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile Ile Leu Met Pro Gly
 115 120 125
 Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala Ala Arg Met Trp Asn
 130 135 140
 Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro Ala Leu Ser Asn Arg
 145 150 155 160
 Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro Ser Ala Thr Leu His
 165 170 175

Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp Gly Trp Lys Lys Ile
 180 185 190

5 Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr Ser Thr Leu Asp Asp
 195 200 205

Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu Ile Thr Phe Arg Gln
 210 215 220

10 Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys Asn Leu Lys Arg Gln
 225 230 235 240

Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu Thr Glu Ala Arg Lys
 15 245 250 255

Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe Gly Lys Lys Tyr Val
 260 265 270

20 Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp Phe Lys Ile Tyr Asp
 275 280 285

Pro Ser Ile Asn Cys Thr Val Asp Glu Met Thr Glu Ala Val Glu Gly
 290 295 300

25 His Ile Thr Thr Glu Ile Val Met Leu Asn Pro Ala Asn Thr Arg Ser
 305 310 315 320

Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu Lys Leu Thr Lys Arg
 30 325 330 335

Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe Gln Glu Ala Pro Leu
 340 345 350

35 Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala Leu Asn Lys Thr Ser
 355 360 365

Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu Asp Phe Asn Tyr Asn
 370 375 380

40 Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala Met Asn Ser Ser Ser
 385 390 395 400

Phe Glu Gly Val Ser Gly His Val Val Phe Asp Ala Ser Gly Ser Arg
 405 410 415

Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly Gly Ser Tyr Lys Lys
 5 420 425 430

Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu Ser Trp Ser Lys Thr
 435 440 445

10 Asp Lys Trp Ile Gly Gly Ser Pro Pro Ala Asp Gln Thr Leu Val Ile
 450 455 460

Lys Thr Phe Arg Phe Leu Ser Gln Lys Leu Phe Ile Ser Val Ser Val
 465 470 475 480

15 Leu Ser Ser Leu Gly Ile Val Leu Ala Val Val Cys Leu Ser Phe Asn
 485 490 495

Ile Tyr Asn Ser His Val Arg Tyr Ile Gln Asn Ser Gln Pro Asn Leu
 20 500 505 510

Asn Asn Leu Thr Ala Val Gly Cys Ser Leu Ala Leu Ala Ala Val Phe
 515 520 525

25 Pro Leu Gly Leu Asp Gly Tyr His Ile Gly Arg Asn Gln Phe Pro Phe
 530 535 540

Val Cys Gln Ala Arg Leu Trp Leu Leu Gly Leu Gly Phe Ser Leu Gly
 545 550 555 560

30 Tyr Gly Ser Met Phe Thr Lys Ile Trp Trp Val His Thr Val Phe Thr
 565 570 575

Lys Lys Glu Glu Lys Lys Glu Trp Arg Lys Thr Leu Glu Pro Trp Lys
 35 580 585 590

Leu Tyr Ala Thr Val Gly Leu Leu Val Gly Met Asp Val Leu Thr Leu
 595 600 605

40 Ala Ile Trp Gln Ile Val Asp Pro Leu His Arg Thr Ile Glu Thr Phe
 610 615 620

Ala Lys Glu Glu Pro Lys Glu Asp Ile Asp Val Ser Ile Leu Pro Gln

	625		630			635		640								
	Leu	Glu	His	Cys	Ser	Ser	Arg	Lys	Met	Asn	Thr	Trp	Leu	Gly	Ile	Phe
					645					650					655	
5	Tyr	Gly	Tyr	Lys	Gly	Leu	Leu	Leu	Leu	Leu	Gly	Ile	Phe	Leu	Ala	Tyr
				660					665					670		
	Glu	Thr	Lys	Ser	Val	Ser	Thr	Glu	Lys	Ile	Asn	Asp	His	Arg	Ala	Val
10			675					680					685			
	Gly	Met	Ala	Ile	Tyr	Asn	Val	Ala	Val	Leu	Cys	Leu	Ile	Thr	Ala	Pro
		690					695				700					
15	Val	Thr	Met	Ile	Leu	Ser	Ser	Gln	Gln	Asp	Ala	Ala	Phe	Ala	Phe	Ala
	705					710				715					720	
	Ser	Leu	Ala	Ile	Val	Phe	Ser	Ser	Tyr	Ile	Thr	Leu	Val	Val	Leu	Phe
				725					730					735		
20	Val	Pro	Lys	Met	Arg	Arg	Leu	Ile	Thr	Arg	Gly	Glu	Trp	Gln	Ser	Glu
			740						745					750		
	Ala	Gln	Asp	Thr	Met	Lys	Thr	Gly	Ser	Ser	Thr	Asn	Asn	Asn	Glu	Glu
25		755						760				765				
	Glu	Lys	Ser	Arg	Leu	Leu	Glu	Lys	Glu	Asn	Arg	Glu	Leu	Glu	Lys	Ile
		770					775				780					
30	Ile	Ala	Glu	Lys	Glu	Glu	Arg	Val	Ser	Glu	Leu	Arg	His	Gln	Leu	Gln
	785					790				795					800	
	Ser	Arg	Gln	Gln	Leu	Arg	Ser	Arg	Arg	His	Pro	Pro	Thr	Pro	Pro	Glu
				805					810					815		
35	Pro	Ser	Gly	Gly	Leu	Pro	Arg	Gly	Pro	Pro	Glu	Pro	Pro	Asp	Arg	Leu
			820					825						830		
	Ser	Cys	Asp	Gly	Ser	Arg	Val	His	Leu	Leu	Tyr	Lys				
40		835						840								

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2895 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Canis familiaris

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..2895

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

ATG CTG CTG CTG CTC CTG CCG CTG GCG CTG GCG CCG CTC TTC CTC CGC	48
Met Leu Leu Leu Leu Leu Pro Leu Ala Leu Ala Pro Leu Phe Leu Arg	
1 5 10 15	
CCC CCG GGC GCG GGC GGG GCA CAG ACC CCC AAC GCC ACC TCG GAA GGT	96
Pro Pro Gly Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly	
20 25 30	
TGC CAG ATC ATA CAC CCG CCT TGG GAA GGG GGT ATC AGG TAC AGG GGC	144
Cys Gln Ile Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly	
35 40 45	
CTG ACT CGT GAC CAG GTG AAG GCT ATC AAC TTC CTG CCG GTG GAC TAT	192
Leu Thr Arg Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr	
50 55 60	
GAG ATT GAG TAT GTG TGC CGG GGA GAG CGA GAG GTG GTG GGG CCC AAG	240
Glu Ile Glu Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys	
65 70 75 80	
GTC CGA AAG TGC CTG GCC AAT GGC TCC TGG ACA GAT ATG GAC ACA CCC	288

	Val	Arg	Lys	Cys	Leu	Ala	Asn	Gly	Ser	Trp	Thr	Asp	Met	Asp	Thr	Pro	
					85					90					95		
	AGC	CGC	TGT	GTC	CGA	ATC	TGT	TCC	AAG	TCA	TAT	TTG	GCC	CTG	GAA	AAT	336
5	Ser	Arg	Cys	Val	Arg	Ile	Cys	Ser	Lys	Ser	Tyr	Leu	Ala	Leu	Glu	Asn	
				100					105					110			
	GGG	AAG	GTC	TTC	CTG	ACG	GGT	GGG	GAC	CTC	CCC	GCT	CTG	GAT	GGA	GCC	384
10	Gly	Lys	Val	Phe	Leu	Thr	Gly	Gly	Asp	Leu	Pro	Ala	Leu	Asp	Gly	Ala	
			115					120					125				
	CGG	GTG	GAT	TTC	CGG	TGT	GAC	CCT	GAC	TTC	CAT	CTT	GTG	GGC	AGC	TCC	432
15	Arg	Val	Asp	Phe	Arg	Cys	Asp	Pro	Asp	Phe	His	Leu	Val	Gly	Ser	Ser	
		130					135				140						
	CGG	AGT	ATC	TGT	AGT	CAG	GGC	CAG	TGG	AGC	ACT	CCC	AAG	CCC	CAC	TGC	480
	Arg	Ser	Ile	Cys	Ser	Gln	Gly	Gln	Trp	Ser	Thr	Pro	Lys	Pro	His	Cys	
	145					150				155					160		
20	CAG	GTG	AGC	CGA	ACG	CCG	CAC	TCA	GAG	CGG	CGA	GCG	GTG	TAC	ATC	GGG	528
	Gln	Val	Ser	Arg	Thr	Pro	His	Ser	Glu	Arg	Arg	Ala	Val	Tyr	Ile	Gly	
					165					170				175			
	GCG	CTG	TTT	CCC	ATG	AGC	GGG	GGC	TGG	CCG	GGG	GGC	CAG	GCC	TGC	CAG	576
25	Ala	Leu	Phe	Pro	Met	Ser	Gly	Gly	Trp	Pro	Gly	Gly	Gln	Ala	Cys	Gln	
				180					185				190				
	CCC	GCG	GTG	GAG	ATG	GCG	CTG	GAG	GAC	GTG	AAT	AGC	CGC	AGG	GAC	ATC	624
30	Pro	Ala	Val	Glu	Met	Ala	Leu	Glu	Asp	Val	Asn	Ser	Arg	Arg	Asp	Ile	
			195					200					205				
	CTG	CCG	GAC	TAC	GAG	CTC	AAG	CTC	ATC	CAC	CAC	GAC	AGC	AAG	TGT	GAC	672
35	Leu	Pro	Asp	Tyr	Glu	Leu	Lys	Leu	Ile	His	His	Asp	Ser	Lys	Cys	Asp	
		210					215					220					
	CCA	GGC	CAA	GCT	ACC	AAG	TAC	CTG	TAT	GAA	CTG	CTC	TAC	AAC	GAC	CCC	720
	Pro	Gly	Gln	Ala	Thr	Lys	Tyr	Leu	Tyr	Glu	Leu	Leu	Tyr	Asn	Asp	Pro	
	225					230				235					240		
40	ATC	AAG	ATC	ATC	CTC	ATG	CCT	GGC	TGC	AGC	TCT	GTC	TCC	ACG	CTT	GTG	768
	Ile	Lys	Ile	Ile	Leu	Met	Pro	Gly	Cys	Ser	Ser	Val	Ser	Thr	Leu	Val	
					245				250						255		

	GCT GAG GCT GCC AGG ATG TGG AAC CTC ATT GTG CTC TCC TAT GGT TCC	816
	Ala Glu Ala Ala Arg Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser	
	260 265 270	
5	AGC TCA CCA GCT CTG TCC AAC CGG CAG CGC TTT CCT ACC TTC TTC CGA	864
	Ser Ser Pro Ala Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg	
	275 280 285	
10	ACT CAT CCC TCG GCC ACG CTC CAC AAC CCT ACG CGA GTG AAG CTC TTT	912
	Thr His Pro Ser Ala Thr Leu His Asn Pro Thr Arg Val Lys Leu Phe	
	290 295 300	
15	GAG AAG TGG GGC TGG AGG AAG ATT GCC ACC ATC CAG CAG ACC ACC GAG	960
	Glu Lys Trp Gly Trp Arg Lys Ile Ala Thr Ile Gln Gln Thr Thr Glu	
	305 310 315 320	
20	GTG TTC ACA TCG ACT CTG GAC GAC CTA GAG GAA CGA GTG AAG GAG GCT	1008
	Val Phe Thr Ser Thr Leu Asp Asp Leu Glu Glu Arg Val Lys Glu Ala	
	325 330 335	
25	GGG ATT GAG ATT ACT TTC CGC CAG AGC TTC TTC TCA GAT CCT GCC GTG	1056
	Gly Ile Glu Ile Thr Phe Arg Gln Ser Phe Phe Ser Asp Pro Ala Val	
	340 345 350	
30	CCT GTC AAG AAC CTC AAG CGC CAG GAT GCC CGA ATC ATC GTG GGA CTT	1104
	Pro Val Lys Asn Leu Lys Arg Gln Asp Ala Arg Ile Ile Val Gly Leu	
	355 360 365	
35	TTC TAT GAG ACT GAA GCC CGG AAA GTG TTC TGT GAG GTA TAC AAG GAG	1152
	Phe Tyr Glu Thr Glu Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu	
	370 375 380	
40	CGG CTC TTT GGG AAG AAG TAT GTG TGG TTC CTC ATT GGG TGG TAT GCT	1200
	Arg Leu Phe Gly Lys Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala	
	385 390 395 400	
45	GAC AAT TGG TTC AAG ACC TAC GAC CCC TCC ATC AAC TGC ACA GTG GAT	1248
	Asp Asn Trp Phe Lys Thr Tyr Asp Pro Ser Ile Asn Cys Thr Val Asp	
	405 410 415	
50	GAG ATG ACC GAG GCT GTG GAA GGC CAC ATC ACC ACT GAG ATT GTC ATG	1296
	Glu Met Thr Glu Ala Val Glu Gly His Ile Thr Thr Glu Ile Val Met	
	420 425 430	

	CTG AAC CCA GCC AAC ACC CGC AGC ATC TCC AAC ATG ACA TCC CAG GAG	1344
	Leu Asn Pro Ala Asn Thr Arg Ser Ile Ser Asn Met Thr Ser Gln Glu	
	435 440 445	
5	TTT GTG GAG AAA CTG ACC AAG AGA CTC AAG AGA CAC CCT GAG GAG ACA	1392
	Phe Val Glu Lys Leu Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr	
	450 455 460	
10	GGC GGC TTC CAG GAG GCA CCG CTG GCC TAT GAT GCC ATC TGG GCC TTG	1440
	Gly Gly Phe Gln Glu Ala Pro Leu Ala Tyr Asp Ala Ile Trp Ala Leu	
	465 470 475 480	
	GCA TTG GCC CTG AAC AAG ACA TCT GGA GGG AGC GGC CGT TCG GGG GTG	1488
15	Ala Leu Ala Leu Asn Lys Thr Ser Gly Gly Ser Gly Arg Ser Gly Val	
	485 490 495	
	CGC CTG GAA GAC TTC AAC TAC AAC AAC CAG ACG ATC ACA GAC CAA ATC	1536
	Arg Leu Glu Asp Phe Asn Tyr Asn Asn Gln Thr Ile Thr Asp Gln Ile	
20	500 505 510	
	TAC CGC GCA ATG AAC TCC TCG TCC TTT GAG GGT GTC TCT GGC CAC GTG	1584
	Tyr Arg Ala Met Asn Ser Ser Ser Phe Glu Gly Val Ser Gly His Val	
	515 520 525	
25	GTG TTT GAT GCC AGC GGC TCA CGG ATG GCC TGG ACT CTG ATT GAG CAG	1632
	Val Phe Asp Ala Ser Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln	
	530 535 540	
30	CTG CAG GGT GGC AGC TAC AAG AAG ATC GGC TAC TAT GAC AGC ACC AAG	1680
	Leu Gln Gly Gly Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys	
	545 550 555 560	
	GAT GAC CTT TCC TGG TCT AAA ACG GAC AAA TGG ATT GGA GGG GCC CCC	1728
35	Asp Asp Leu Ser Trp Ser Lys Thr Asp Lys Trp Ile Gly Gly Ala Pro	
	565 570 575	
	CCG GCC GAC CAG ACC CTG GTC ATC AAG ACA TTT CGC TTC ATG TCA CAG	1776
	Pro Ala Asp Gln Thr Leu Val Ile Lys Thr Phe Arg Phe Met Ser Gln	
40	580 585 590	
	AAG CTC TTC ATT TCA GTC TCT GTC CTC TCC AGC CTG GGC ATT GTC CTG	1824
	Lys Leu Phe Ile Ser Val Ser Val Leu Ser Ser Leu Gly Ile Val Leu	

	595	600	605	
	GCT GTG GTC TGT CTG TCC TTT AAC ATC TAC AAC TCT CAT GTC CGT TAC	1872		
	Ala Val Val Cys Leu Ser Phe Asn Ile Tyr Asn Ser His Val Arg Tyr			
5	610	615	620	
	ATC CAG AAC TCC CAG CCC AAC TTG AAC AAT CTG ACT GCT GTG GGC TGC	1920		
	Ile Gln Asn Ser Gln Pro Asn Leu Asn Asn Leu Thr Ala Val Gly Cys			
	625	630	635	640
10	TCC CTG GCA TTG GCT GCC GTC TTC CCC CTG GGG CTA GAT GGG TAC CAC	1968		
	Ser Leu Ala Leu Ala Ala Val Phe Pro Leu Gly Leu Asp Gly Tyr His			
	645	650	655	
15	ATC GGG AGA AGC CAG TTT CCT TTT GTG TGT CAG GCA CGC CTC TGG CTC	2016		
	Ile Gly Arg Ser Gln Phe Pro Phe Val Cys Gln Ala Arg Leu Trp Leu			
	660	665	670	
	CTG GGT CTG GGC TTC AGT CTG GGC TAT GGC TCC ATG TTC ACG AAG ATC	2064		
20	Leu Gly Leu Gly Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr Lys Ile			
	675	680	685	
	TGG TGG GTC CAC ACG GTC TTC ACT AAG AAG GAG GAG AAG AAG GAG TGG	2112		
	Trp Trp Val His Thr Val Phe Thr Lys Lys Glu Glu Lys Lys Glu Trp			
25	690	695	700	
	AGG AAG ACC CTG GAG CCC TGG AAG CTG TAC ACC ACA GTG GGC TTG CTA	2160		
	Arg Lys Thr Leu Glu Pro Trp Lys Leu Tyr Thr Thr Val Gly Leu Leu			
	705	710	715	720
30	GTG GGC ATG GAT GTC CTC ACT CTT GCC ATT TGG CAG ATG GTA GAC CCC	2208		
	Val Gly Met Asp Val Leu Thr Leu Ala Ile Trp Gln Met Val Asp Pro			
	725	730	735	
35	TTG CAC CGG ACC ATT GAG ACT TTT GCC AAG GAG GAA CCA AAG GAA GAT	2256		
	Leu His Arg Thr Ile Glu Thr Phe Ala Lys Glu Glu Pro Lys Glu Asp			
	740	745	750	
	ATT GAT GTG TCC ATC CTG CCC CAG CTG GAG CAC TGC AGC TCC AAG AAA	2304		
40	Ile Asp Val Ser Ile Leu Pro Gln Leu Glu His Cys Ser Ser Lys Lys			
	755	760	765	
	ATG AAC ACC TGG CTT GGC ATT TTC TAT GGT TAC AAG GGG CTG CTG CTG	2352		

	Met	Asn	Thr	Trp	Leu	Gly	Ile	Phe	Tyr	Gly	Tyr	Lys	Gly	Leu	Leu	Leu	
	770						775					780					
	CTG	CTA	GGC	ATC	TTT	CTT	GCT	TAT	GAG	ACC	AAG	AGC	GTG	TCT	ACT	GAG	2400
5	Leu	Leu	Gly	Ile	Phe	Leu	Ala	Tyr	Glu	Thr	Lys	Ser	Val	Ser	Thr	Glu	
	785					790					795					800	
	AAG	ATC	AAT	GAC	CAC	CGG	GCT	GTG	GGC	ATG	GCC	ATG	TAC	AAC	GTG	GCG	2448
	Lys	Ile	Asn	Asp	His	Arg	Ala	Val	Gly	Met	Ala	Met	Tyr	Asn	Val	Ala	
10					805					810					815		
	GTC	CTG	TGC	CTC	ATC	ACT	GCC	CCG	GTC	ACC	ATG	ATC	CTG	TCC	AGC	CAG	2496
	Val	Leu	Cys	Leu	Ile	Thr	Ala	Pro	Val	Thr	Met	Ile	Leu	Ser	Ser	Gln	
					820					825					830		
15																	
	CAG	GAT	GCA	GCT	TTC	GCC	TTT	GCA	GCT	CTT	GCC	ATA	GTG	TTC	TCC	TCC	2544
	Gln	Asp	Ala	Ala	Phe	Ala	Phe	Ala	Ala	Leu	Ala	Ile	Val	Phe	Ser	Ser	
					835					840					845		
20																	
	TAC	ATC	ACT	CTG	GTC	GTT	CTG	TTC	GTG	CCG	AAG	ATG	CGC	AGG	TTG	ATC	2592
	Tyr	Ile	Thr	Leu	Val	Val	Leu	Phe	Val	Pro	Lys	Met	Arg	Arg	Leu	Ile	
					850					855					860		
	ACC	CGG	GGT	GAG	TGG	CAG	TCG	GAG	GCG	CAG	GAT	ACC	ATG	AAA	ACG	GGG	2640
25	Thr	Arg	Gly	Glu	Trp	Gln	Ser	Glu	Ala	Gln	Asp	Thr	Met	Lys	Thr	Gly	
	865					870					875					880	
	TCG	TCG	ACC	AAC	AAC	AAT	GAG	GAA	GAG	AAG	TCC	CGA	CTG	TTG	GAG	AAG	2688
	Ser	Ser	Thr	Asn	Asn	Asn	Glu	Glu	Glu	Lys	Ser	Arg	Leu	Leu	Glu	Lys	
30						885				890					895		
	GAG	AAC	CGG	GAG	CTG	GAG	AAG	ATC	ATT	GCT	GAG	AAA	GAG	GAG	CGA	GTG	2736
	Glu	Asn	Arg	Glu	Leu	Glu	Lys	Ile	Ile	Ala	Glu	Lys	Glu	Glu	Arg	Val	
					900					905					910		
35																	
	TCC	GAG	CTG	CGC	CAT	CAG	CTT	CGT	TCT	CGG	CAG	CAG	CTG	CGC	CCT	CGG	2784
	Ser	Glu	Leu	Arg	His	Gln	Leu	Arg	Ser	Arg	Gln	Gln	Leu	Arg	Pro	Arg	
					915					920					925		
40																	
	CGT	CAC	CCC	CCG	ACG	CCC	CCA	GAC	CCC	TCA	GGG	GGC	CTG	CCC	AGG	GGA	2832
	Arg	His	Pro	Pro	Thr	Pro	Pro	Asp	Pro	Ser	Gly	Gly	Leu	Pro	Arg	Gly	
					930					935					940		

CCC CAT GAG CCC CCT GAC CGG CTC AGC TGT GAC GGG AGC CGG GTT CAC 2880
 Pro His Glu Pro Pro Asp Arg Leu Ser Cys Asp Gly Ser Arg Val His
 945 950 955 960

5 TTG CTG TAC AAG TGA 2895
 Leu Leu Tyr Lys *
 965

10 (2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 964 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

20 Met Leu Leu Leu Leu Leu Pro Leu Ala Leu Ala Pro Leu Phe Leu Arg
 1 5 10 15

Pro Pro Gly Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly
 25 20 25 30

Cys Gln Ile Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly
 35 40 45

30 Leu Thr Arg Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr
 50 55 60

Glu Ile Glu Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys
 65 70 75 80

35 Val Arg Lys Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro
 85 90 95

Ser Arg Cys Val Arg Ile Cys Ser Lys Ser Tyr Leu Ala Leu Glu Asn
 40 100 105 110

Gly Lys Val Phe Leu Thr Gly Gly Asp Leu Pro Ala Leu Asp Gly Ala
 115 120 125

Arg Val Asp Phe Arg Cys Asp Pro Asp Phe His Leu Val Gly Ser Ser
 130 135 140

5 Arg Ser Ile Cys Ser Gln Gly Gln Trp Ser Thr Pro Lys Pro His Cys
 145 150 155 160

Gln Val Ser Arg Thr Pro His Ser Glu Arg Arg Ala Val Tyr Ile Gly
 165 170 175

10 Ala Leu Phe Pro Met Ser Gly Gly Trp Pro Gly Gly Gln Ala Cys Gln
 180 185 190

Pro Ala Val Glu Met Ala Leu Glu Asp Val Asn Ser Arg Arg Asp Ile
 15 195 200 205

Leu Pro Asp Tyr Glu Leu Lys Leu Ile His His Asp Ser Lys Cys Asp
 210 215 220

20 Pro Gly Gln Ala Thr Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn Asp Pro
 225 230 235 240

Ile Lys Ile Ile Leu Met Pro Gly Cys Ser Ser Val Ser Thr Leu Val
 245 250 255

25 Ala Glu Ala Ala Arg Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser
 260 265 270

Ser Ser Pro Ala Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg
 30 275 280 285

Thr His Pro Ser Ala Thr Leu His Asn Pro Thr Arg Val Lys Leu Phe
 290 295 300

35 Glu Lys Trp Gly Trp Arg Lys Ile Ala Thr Ile Gln Gln Thr Thr Glu
 305 310 315 320

Val Phe Thr Ser Thr Leu Asp Asp Leu Glu Glu Arg Val Lys Glu Ala
 325 330 335

40 Gly Ile Glu Ile Thr Phe Arg Gln Ser Phe Phe Ser Asp Pro Ala Val
 340 345 350

Pro Val Lys Asn Leu Lys Arg Gln Asp Ala Arg Ile Ile Val Gly Leu
 355 360 365

Phe Tyr Glu Thr Glu Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu
 5 370 375 380

Arg Leu Phe Gly Lys Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala
 385 390 395 400

10 Asp Asn Trp Phe Lys Thr Tyr Asp Pro Ser Ile Asn Cys Thr Val Asp
 405 410 415

Glu Met Thr Glu Ala Val Glu Gly His Ile Thr Thr Glu Ile Val Met
 420 425 430

15 Leu Asn Pro Ala Asn Thr Arg Ser Ile Ser Asn Met Thr Ser Gln Glu
 435 440 445

Phe Val Glu Lys Leu Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr
 20 450 455 460

Gly Gly Phe Gln Glu Ala Pro Leu Ala Tyr Asp Ala Ile Trp Ala Leu
 465 470 475 480

25 Ala Leu Ala Leu Asn Lys Thr Ser Gly Gly Ser Gly Arg Ser Gly Val
 485 490 495

Arg Leu Glu Asp Phe Asn Tyr Asn Asn Gln Thr Ile Thr Asp Gln Ile
 500 505 510

30 Tyr Arg Ala Met Asn Ser Ser Ser Phe Glu Gly Val Ser Gly His Val
 515 520 525

Val Phe Asp Ala Ser Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln
 35 530 535 540

Leu Gln Gly Gly Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys
 545 550 555 560

40 Asp Asp Leu Ser Trp Ser Lys Thr Asp Lys Trp Ile Gly Gly Ala Pro
 565 570 575

Pro Ala Asp Gln Thr Leu Val Ile Lys Thr Phe Arg Phe Met Ser Gln

	580	585	590
	Lys Leu Phe Ile Ser Val Ser Val Leu Ser Ser Leu Gly Ile Val Leu		
	595	600	605
5	Ala Val Val Cys Leu Ser Phe Asn Ile Tyr Asn Ser His Val Arg Tyr		
	610	615	620
	Ile Gln Asn Ser Gln Pro Asn Leu Asn Asn Leu Thr Ala Val Gly Cys		
10	625	630	635 640
	Ser Leu Ala Leu Ala Ala Val Phe Pro Leu Gly Leu Asp Gly Tyr His		
	645	650	655
15	Ile Gly Arg Ser Gln Phe Pro Phe Val Cys Gln Ala Arg Leu Trp Leu		
	660	665	670
	Leu Gly Leu Gly Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr Lys Ile		
	675	680	685
20	Trp Trp Val His Thr Val Phe Thr Lys Lys Glu Glu Lys Lys Glu Trp		
	690	695	700
	Arg Lys Thr Leu Glu Pro Trp Lys Leu Tyr Thr Thr Val Gly Leu Leu		
25	705	710	715 720
	Val Gly Met Asp Val Leu Thr Leu Ala Ile Trp Gln Met Val Asp Pro		
	725	730	735
30	Leu His Arg Thr Ile Glu Thr Phe Ala Lys Glu Glu Pro Lys Glu Asp		
	740	745	750
	Ile Asp Val Ser Ile Leu Pro Gln Leu Glu His Cys Ser Ser Lys Lys		
	755	760	765
35	Met Asn Thr Trp Leu Gly Ile Phe Tyr Gly Tyr Lys Gly Leu Leu Leu		
	770	775	780
	Leu Leu Gly Ile Phe Leu Ala Tyr Glu Thr Lys Ser Val Ser Thr Glu		
40	785	790	795 800
	Lys Ile Asn Asp His Arg Ala Val Gly Met Ala Met Tyr Asn Val Ala		
	805	810	815

Val Leu Cys Leu Ile Thr Ala Pro Val Thr Met Ile Leu Ser Ser Gln
820 825 830

5 Gln Asp Ala Ala Phe Ala Phe Ala Ala Leu Ala Ile Val Phe Ser Ser
835 840 845

Tyr Ile Thr Leu Val Val Leu Phe Val Pro Lys Met Arg Arg Leu Ile
850 855 860

10 Thr Arg Gly Glu Trp Gln Ser Glu Ala Gln Asp Thr Met Lys Thr Gly
865 870 875 880

Ser Ser Thr Asn Asn Asn Glu Glu Glu Lys Ser Arg Leu Leu Glu Lys
15 885 890 895

Glu Asn Arg Glu Leu Glu Lys Ile Ile Ala Glu Lys Glu Glu Arg Val
900 905 910

20 Ser Glu Leu Arg His Gln Leu Arg Ser Arg Gln Gln Leu Arg Pro Arg
915 920 925

Arg His Pro Pro Thr Pro Pro Asp Pro Ser Gly Gly Leu Pro Arg Gly
930 935 940

25 Pro His Glu Pro Pro Asp Arg Leu Ser Cys Asp Gly Ser Arg Val His
945 950 955 960

Leu Leu Tyr Lys

30

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 1737 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..1737

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

5
 10
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ATG TTG CTG CTG CTG CTA CTG GCG CCA CTC TTC CTC CGC CCC CCG GGC	48
Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly	
1 5 10 15	
GCG GGC GGG GCG CAG ACC CCC AAC GCC ACC TCA GAA GGT TGC CAG ATC	96
Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile	
20 25 30	
ATA CAC CCG CCC TGG GAA GGG GGC ATC AGG TAC CGG GGC CTG ACT CGG	144
Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg	
35 40 45	
GAC CAG GTG AAG GCT ATC AAC TTC CTG CCA GTG GAC TAT GAG ATT GAG	192
Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu	
50 55 60	
TAT GTG TGC CGG GGG GAG CGC GAG GTG GTG GGG CCC AAG GTC CGC AAG	240
Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys	
65 70 75 80	
TGC CTG GCC AAC GGC TCC TGG ACA GAT ATG GAC ACA CCC AGC CGC TGT	288
Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys	
85 90 95	
GTC CGA ATC TGC TCC AAG TCT TAT TTG ACC CTG GAA AAT GGG AAG GTT	336
Val Arg Ile Cys Ser Lys Ser Tyr Leu Thr Leu Glu Asn Gly Lys Val	
100 105 110	
TTC CTG ACG GGT GGG GAC CTC CCA GCT CTG GAC GGA GCC CGG GTG GAT	384
Phe Leu Thr Gly Gly Asp Leu Pro Ala Leu Asp Gly Ala Arg Val Asp	
115 120 125	

	TTC CGG TGT GAC CCC GAC TTC CAT CTG GTG GGC AGC TCC CGG AGC ATC	432
	Phe Arg Cys Asp Pro Asp Phe His Leu Val Gly Ser Ser Arg Ser Ile	
	130 135 140	
5	TGT AGT CAG GGC CAG TGG AGC ACC CCC AAG CCC CAC TGC CAG GTG AAT	480
	Cys Ser Gln Gly Gln Trp Ser Thr Pro Lys Pro His Cys Gln Val Asn	
	145 150 155 160	
10	CGA ACG CCA CAC TCA GAA CGG CGC GCA GTG TAC ATC GGG GCA CTG TTT	528
	Arg Thr Pro His Ser Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe	
	165 170 175	
15	CCC ATG AGC GGG GGC TGG CCA GGG GGC CAG GCC TGC CAG CCC GCG GTG	576
	Pro Met Ser Gly Gly Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val	
	180 185 190	
20	GAG ATG GCG CTG GAG GAC GTG AAT AGC CGC AGG GAC ATC CTG CCG GAC	624
	Glu Met Ala Leu Glu Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp	
	195 200 205	
25	TAT GAG CTC AAG CTC ATC CAC CAC GAC AGC AAG TGT GAT CCA GGC CAA	672
	Tyr Glu Leu Lys Leu Ile His His Asp Ser Lys Cys Asp Pro Gly Gln	
	210 215 220	
30	GCC ACC AAG TAC CTA TAT GAG CTG CTC TAC AAC GAC CCT ATC AAG ATC	720
	Ala Thr Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile	
	225 230 235 240	
35	ATC CTT ATG CCT GGC TGC AGC TCT GTC TCC ACG CTG GTG GCT GAG GCT	768
	Ile Leu Met Pro Gly Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala	
	245 250 255	
40	GCT AGG ATG TGG AAC CTC ATT GTG CTT TCC TAT GGC TCC AGC TCA CCA	816
	Ala Arg Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro	
	260 265 270	
45	GCC CTG TCA AAC CGG CAG CGT TTC CCC ACT TTC TTC CGA ACG CAC CCA	864
	Ala Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro	
	275 280 285	
50	TCA GCC ACA CTC CAC AAC CCT ACC CGC GTG AAA CTC TTT GAA AAG TGG	912
	Ser Ala Thr Leu His Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp	
	290 295 300	

	GGC TGG AAG AAG ATT GCT ACC ATC CAG CAG ACC ACT GAG GTC TTC ACT	960
	Gly Trp Lys Lys Ile Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr	
	305 310 315 320	
5	TCG ACT CTG GAC GAC CTG GAG GAA CGA GTG AAG GAG GCT GGA ATT GAG	1008
	Ser Thr Leu Asp Asp Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu	
	325 330 335	
10	ATT ACT TTC CGC CAG AGT TTC TTC TCA GAT CCA GCT GTG CCC GTC AAA	1056
	Ile Thr Phe Arg Gln Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys	
	340 345 350	
	AAC CTG AAG CGC CAG GAT GCC CGA ATC ATC GTG GGA CTT TTC TAT GAG	1104
15	Asn Leu Lys Arg Gln Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu	
	355 360 365	
	ACT GAA GCC CGG AAA GTT TTT TGT GAG GTG TAC AAG GAG CGT CTC TTT	1152
	Thr Glu Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe	
20	370 375 380	
	GGG AAG AAG TAC GTC TGG TTC CTC ATT GGG TGG TAT GCT GAC AAT TGG	1200
	Gly Lys Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp	
	385 390 395 400	
25	TTC AAG ATC TAC GAC CCT TCT ATC AAC TGC ACA GTG GAT GAG ATG ACT	1248
	Phe Lys Ile Tyr Asp Pro Ser Ile Asn Cys Thr Val Asp Glu Met Thr	
	405 410 415	
30	GAG GCG GTG GAG GGC CAC ATC ACA ACT GAG ATT GTC ATG CTG AAT CCT	1296
	Glu Ala Val Glu Gly His Ile Thr Thr Glu Ile Val Met Leu Asn Pro	
	420 425 430	
	GCC AAT ACC CGC AGC ATT TCC AAC ATG ACA TCC CAG GAA TTT GTG GAG	1344
35	Ala Asn Thr Arg Ser Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu	
	435 440 445	
	AAA CTA ACC AAG CGA CTG AAA AGA CAC CCT GAG GAG ACA GGA GGC TTC	1392
	Lys Leu Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe	
40	450 455 460	
	CAG GAG GCA CCG CTG GCC TAT GAT GCC ATC TGG GCC TTG GCA CTG GCC	1440
	Gln Glu Ala Pro Leu Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala	

	465	470	475	480	
	CTG AAC AAG ACA TCT GGA GGA GGC GGC CGT TCT GGT GTG CGC CTG GAG				1488
	Leu Asn Lys Thr Ser Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu				
5		485	490	495	
	GAC TTC AAC TAC AAC AAC CAG ACC ATT ACC GAC CAA ATC TAC CGG GCA				1536
	Asp Phe Asn Tyr Asn Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala				
		500	505	510	
10	ATG AAC TCT TCG TCC TTT GAG GGT GTC TCT GGC CAT GTG GTG TTT GAT				1584
	Met Asn Ser Ser Ser Phe Glu Gly Val Ser Gly His Val Val Phe Asp				
		515	520	525	
15	GCC AGC GGC TCT CGG ATG GCA TGG ACG CTT ATC GAG CAG CTT CAG GGT				1632
	Ala Ser Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly				
		530	535	540	
	GGC AGC TAC AAG AAG ATT GGC TAC TAT GAC AGC ACC AAG GAT GAT CTT				1680
20	Gly Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu				
		545	550	555	560
	TCC TGG TCC AAA ACA GAT AAA TGG ATT GTT ATA TCC AGA ACT CAC AGC				1728
	Ser Trp Ser Lys Thr Asp Lys Trp Ile Val Ile Ser Arg Thr His Ser				
25		565	570	575	
	CCA ACC TGA				1737
	Pro Thr *				

30

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 578 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly

1	5	10	15
Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile	20	25	30
Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg	35	40	45
Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu	50	55	60
Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys	65	70	75
Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys	85	90	95
Val Arg Ile Cys Ser Lys Ser Tyr Leu Thr Leu Glu Asn Gly Lys Val	100	105	110
Phe Leu Thr Gly Gly Asp Leu Pro Ala Leu Asp Gly Ala Arg Val Asp	115	120	125
Phe Arg Cys Asp Pro Asp Phe His Leu Val Gly Ser Ser Arg Ser Ile	130	135	140
Cys Ser Gln Gly Gln Trp Ser Thr Pro Lys Pro His Cys Gln Val Asn	145	150	155
Arg Thr Pro His Ser Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe	165	170	175
Pro Met Ser Gly Gly Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val	180	185	190
Glu Met Ala Leu Glu Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp	195	200	205
Tyr Glu Leu Lys Leu Ile His His Asp Ser Lys Cys Asp Pro Gly Gln	210	215	220
Ala Thr Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile	225	230	235
			240

Ile Leu Met Pro Gly Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala
245 250 255

5 Ala Arg Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro
260 265 270

Ala Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro
275 280 285

10 Ser Ala Thr Leu His Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp
290 295 300

Gly Trp Lys Lys Ile Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr
15 305 310 315 320

Ser Thr Leu Asp Asp Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu
325 330 335

20 Ile Thr Phe Arg Gln Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys
340 345 350

Asn Leu Lys Arg Gln Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu
355 360 365

25 Thr Glu Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe
370 375 380

Gly Lys Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp
30 385 390 395 400

Phe Lys Ile Tyr Asp Pro Ser Ile Asn Cys Thr Val Asp Glu Met Thr
405 410 415

35 Glu Ala Val Glu Gly His Ile Thr Thr Glu Ile Val Met Leu Asn Pro
420 425 430

Ala Asn Thr Arg Ser Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu
435 440 445

40 Lys Leu Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe
450 455 460

Gln Glu Ala Pro Leu Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala
 465 470 475 480
 Leu Asn Lys Thr Ser Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu
 5 485 490 495
 Asp Phe Asn Tyr Asn Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala
 500 505 510
 Met Asn Ser Ser Ser Phe Glu Gly Val Ser Gly His Val Val Phe Asp
 10 515 520 525
 Ala Ser Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly
 530 535 540
 Gly Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu
 15 545 550 555 560
 Ser Trp Ser Lys Thr Asp Lys Trp Ile Val Ile Ser Arg Thr His Ser
 20 565 570 575
 Pro Thr

25

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1386 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: cDNA to mRNA

35

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..1386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

5 ATG GGG CCC GGG GCC CCT TTT GCC CGG GTG GGG TGG CCA CTG CCG CTT 48
Met Gly Pro Gly Ala Pro Phe Ala Arg Val Gly Trp Pro Leu Pro Leu
1 5 10 15

10 CTG GTT GTG ATG GCG GCA GGG GTG GCT CCG GTG TGG GCC TCC CAC TCC 96
Leu Val Val Met Ala Ala Gly Val Ala Pro Val Trp Ala Ser His Ser
20 25 30

15 CCC CAT CTC CCG CGG CCT CAC TCG CGG GTC CCC CCG CAC CCC TCC TCA 144
Pro His Leu Pro Arg Pro His Ser Arg Val Pro Pro His Pro Ser Ser
35 40 45

20 GAA CGG CGC GCA GTG TAC ATC GGG GCA CTG TTT CCC ATG AGC GGG GGC 192
Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe Pro Met Ser Gly Gly
50 55 60

TGG CCA GGG GGC CAG GCC TGC CAG CCC GCG GTG GAG ATG GCG CTG GAG 240
Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val Glu Met Ala Leu Glu
65 70 75 80

25 GAC GTG AAT AGC CGC AGG GAC ATC CTG CCG GAC TAT GAG CTC AAG CTC 288
Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp Tyr Glu Leu Lys Leu
85 90 95

30 ATC CAC CAC GAC AGC AAG TGT GAT CCA GGC CAA GCC ACC AAG TAC CTA 336
Ile His His Asp Ser Lys Cys Asp Pro Gly Gln Ala Thr Lys Tyr Leu
100 105 110

35 TAT GAG CTG CTC TAC AAC GAC CCT ATC AAG ATC ATC CTT ATG CCT GGC 384
Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile Ile Leu Met Pro Gly
115 120 125

TGC AGC TCT GTC TCC ACG CTG GTG GCT GAG GCT GCT AGG ATG TGG AAC 432
Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala Ala Arg Met Trp Asn
40 130 135 140

CTC ATT GTG CTT TCC TAT GGC TCC AGC TCA CCA GCC CTG TCA AAC CGG 480
Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro Ala Leu Ser Asn Arg

	145	150	155	160	
	CAG CGT TTC CCC ACT TTC TTC CGA ACG CAC CCA TCA GCC ACA CTC CAC				528
	Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro Ser Ala Thr Leu His				
5		165	170	175	
	AAC CCT ACC CGC GTG AAA CTC TTT GAA AAG TGG GGC TGG AAG AAG ATT				576
	Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp Gly Trp Lys Lys Ile				
		180	185	190	
10	GCT ACC ATC CAG CAG ACC ACT GAG GTC TTC ACT TCG ACT CTG GAC GAC				624
	Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr Ser Thr Leu Asp Asp				
		195	200	205	
15	CTG GAG GAA CGA GTG AAG GAG GCT GGA ATT GAG ATT ACT TTC CGC CAG				672
	Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu Ile Thr Phe Arg Gln				
		210	215	220	
	AGT TTC TTC TCA GAT CCA GCT GTG CCC GTC AAA AAC CTG AAG CGC CAG				720
20	Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys Asn Leu Lys Arg Gln				
		225	230	235	240
	GAT GCC CGA ATC ATC GTG GGA CTT TTC TAT GAG ACT GAA GCC CGG AAA				768
	Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu Thr Glu Ala Arg Lys				
25		245	250	255	
	GTT TTT TGT GAG GTG TAC AAG GAG CGT CTC TTT GGG AAG AAG TAC GTC				816
	Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe Gly Lys Lys Tyr Val				
		260	265	270	
30	TGG TTC CTC ATT GGG TGG TAT GCT GAC AAT TGG TTC AAG ATC TAC GAC				864
	Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp Phe Lys Ile Tyr Asp				
		275	280	285	
35	CCT TCT ATC AAC TGC ACA GTG GAT GAG ATG ACT GAG GCG GTG GAG GGC				912
	Pro Ser Ile Asn Cys Thr Val Asp Glu Met Thr Glu Ala Val Glu Gly				
		290	295	300	
	CAC ATC ACA ACT GAG ATT GTC ATG CTG AAT CCT GCC AAT ACC CGC AGC				960
40	His Ile Thr Thr Glu Ile Val Met Leu Asn Pro Ala Asn Thr Arg Ser				
		305	310	315	320
	ATT TCC AAC ATG ACA TCC CAG GAA TTT GTG GAG AAA CTA ACC AAG CGA				1008

	Ile	Ser	Asn	Met	Thr	Ser	Gln	Glu	Phe	Val	Glu	Lys	Leu	Thr	Lys	Arg	
					325					330					335		
	CTG	AAA	AGA	CAC	CCT	GAG	GAG	ACA	GGA	GGC	TTC	CAG	GAG	GCA	CCG	CTG	1056
5	Leu	Lys	Arg	His	Pro	Glu	Glu	Thr	Gly	Gly	Phe	Gln	Glu	Ala	Pro	Leu	
				340					345					350			
	GCC	TAT	GAT	GCC	ATC	TGG	GCC	TTG	GCA	CTG	GCC	CTG	AAC	AAG	ACA	TCT	1104
	Ala	Tyr	Asp	Ala	Ile	Trp	Ala	Leu	Ala	Leu	Ala	Leu	Asn	Lys	Thr	Ser	
10			355					360					365				
	GGA	GGA	GGC	GGC	CGT	TCT	GGT	GTG	CGC	CTG	GAG	GAC	TTC	AAC	TAC	AAC	1152
	Gly	Gly	Gly	Gly	Arg	Ser	Gly	Val	Arg	Leu	Glu	Asp	Phe	Asn	Tyr	Asn	
			370					375					380				
15	AAC	CAG	ACC	ATT	ACC	GAC	CAA	ATC	TAC	CGG	GCA	ATG	AAC	TCT	TCG	TCC	1200
	Asn	Gln	Thr	Ile	Thr	Asp	Gln	Ile	Tyr	Arg	Ala	Met	Asn	Ser	Ser	Ser	
			385					390					395			400	
20	TTT	GAG	GGT	GTC	TCT	GGC	CAT	GTG	GTG	TTT	GAT	GCC	AGC	GGC	TCT	CGG	1248
	Phe	Glu	Gly	Val	Ser	Gly	His	Val	Val	Phe	Asp	Ala	Ser	Gly	Ser	Arg	
				405						410					415		
	ATG	GCA	TGG	ACG	CTT	ATC	GAG	CAG	CTT	CAG	GGT	GGC	AGC	TAC	AAG	AAG	1296
25	Met	Ala	Trp	Thr	Leu	Ile	Glu	Gln	Leu	Gln	Gly	Gly	Ser	Tyr	Lys	Lys	
				420					425					430			
	ATT	GGC	TAC	TAT	GAC	AGC	ACC	AAG	GAT	GAT	CTT	TCC	TGG	TCC	AAA	ACA	1344
	Ile	Gly	Tyr	Tyr	Asp	Ser	Thr	Lys	Asp	Asp	Leu	Ser	Trp	Ser	Lys	Thr	
30			435					440					445				
	GAT	AAA	TGG	ATT	GTT	ATA	TCC	AGA	ACT	CAC	AGC	CCA	ACC	TGA			1386
	Asp	Lys	Trp	Ile	Val	Ile	Ser	Arg	Thr	His	Ser	Pro	Thr	*			
			450					455					460				
35																	

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 461 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

```

Met Gly Pro Gly Ala Pro Phe Ala Arg Val Gly Trp Pro Leu Pro Leu
5      1              5              10              15

Leu Val Val Met Ala Ala Gly Val Ala Pro Val Trp Ala Ser His Ser
              20              25              30

10  Pro His Leu Pro Arg Pro His Ser Arg Val Pro Pro His Pro Ser Ser
              35              40              45

Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe Pro Met Ser Gly Gly
              50              55              60

15  Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val Glu Met Ala Leu Glu
              65              70              75              80

Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp Tyr Glu Leu Lys Leu
20              85              90              95

Ile His His Asp Ser Lys Cys Asp Pro Gly Gln Ala Thr Lys Tyr Leu
              100             105             110

25  Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile Ile Leu Met Pro Gly
              115             120             125

Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala Ala Arg Met Trp Asn
              130             135             140

30  Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro Ala Leu Ser Asn Arg
              145             150             155             160

Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro Ser Ala Thr Leu His
35              165             170             175

Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp Gly Trp Lys Lys Ile
              180             185             190

40  Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr Ser Thr Leu Asp Asp
              195             200             205

Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu Ile Thr Phe Arg Gln

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	210	215	220	
	Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys Asn Leu Lys Arg Gln			
	225	230	235	240
5	Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu Thr Glu Ala Arg Lys			
	245	250	255	
	Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe Gly Lys Lys Tyr Val			
10	260	265	270	
	Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp Phe Lys Ile Tyr Asp			
	275	280	285	
15	Pro Ser Ile Asn Cys Thr Val Asp Glu Met Thr Glu Ala Val Glu Gly			
	290	295	300	
	His Ile Thr Thr Glu Ile Val Met Leu Asn Pro Ala Asn Thr Arg Ser			
	305	310	315	320
20	Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu Lys Leu Thr Lys Arg			
	325	330	335	
	Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe Gln Glu Ala Pro Leu			
25	340	345	350	
	Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala Leu Asn Lys Thr Ser			
	355	360	365	
30	Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu Asp Phe Asn Tyr Asn			
	370	375	380	
	Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala Met Asn Ser Ser Ser			
	385	390	395	400
35	Phe Glu Gly Val Ser Gly His Val Val Phe Asp Ala Ser Gly Ser Arg			
	405	410	415	
	Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly Gly Ser Tyr Lys Lys			
40	420	425	430	
	Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu Ser Trp Ser Lys Thr			
	435	440	445	

Asp Lys Trp Ile Val Ile Ser Arg Thr His Ser Pro Thr
 450 455 460

5

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1746 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: cDNA to mRNA

15

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

20

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Canis familiaris

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..1746

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

ATG CTG CTG CTG CTC CTG CCG CTG GCG CTG GCG CCG CTC TTC CTC CGC	48
Met Leu Leu Leu Leu Leu Pro Leu Ala Leu Ala Pro Leu Phe Leu Arg	
1 5 10 15	
CCC CCG GGC GCG GGC GGG GCA CAG ACC CCC AAC GCC ACC TCG GAA GGT	96
Pro Pro Gly Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly	
35 20 25 30	
TGC CAG ATC ATA CAC CCG CCT TGG GAA GGG GGT ATC AGG TAC AGG GGC	144
Cys Gln Ile Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly	
35 40 45	
CTG ACT CGT GAC CAG GTG AAG GCT ATC AAC TTC CTG CCG GTG GAC TAT	192
Leu Thr Arg Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr	
50 55 60	

40

	GAG ATT GAG TAT GTG TGC CGG GGA GAG CGA GAG GTG GTG GGG CCC AAG	240
	Glu Ile Glu Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys	
	65 70 75 80	
5	GTC CGA AAG TGC CTG GCC AAT GGC TCC TGG ACA GAT ATG GAC ACA CCC	288
	Val Arg Lys Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro	
	85 90 95	
10	AGC CGC TGT GTC CGA ATC TGT TCC AAG TCA TAT TTG GCC CTG GAA AAT	336
	Ser Arg Cys Val Arg Ile Cys Ser Lys Ser Tyr Leu Ala Leu Glu Asn	
	100 105 110	
15	GGG AAG GTC TTC CTG ACG GGT GGG GAC CTC CCC GCT CTG GAT GGA GCC	384
	Gly Lys Val Phe Leu Thr Gly Gly Asp Leu Pro Ala Leu Asp Gly Ala	
	115 120 125	
20	CGG GTG GAT TTC CGG TGT GAC CCT GAC TTC CAT CTT GTG GGC AGC TCC	432
	Arg Val Asp Phe Arg Cys Asp Pro Asp Phe His Leu Val Gly Ser Ser	
	130 135 140	
25	CGG AGT ATC TGT AGT CAG GGC CAG TGG AGC ACT CCC AAG CCC CAC TGC	480
	Arg Ser Ile Cys Ser Gln Gly Gln Trp Ser Thr Pro Lys Pro His Cys	
	145 150 155 160	
30	CAG GTG AGC CGA ACG CCG CAC TCA GAG CGG CGA GCG GTG TAC ATC GGG	528
	Gln Val Ser Arg Thr Pro His Ser Glu Arg Arg Ala Val Tyr Ile Gly	
	165 170 175	
35	GCG CTG TTT CCC ATG AGC GGG GGC TGG CCG GGG GGC CAG GCC TGC CAG	576
	Ala Leu Phe Pro Met Ser Gly Gly Trp Pro Gly Gly Gln Ala Cys Gln	
	180 185 190	
40	CCC GCG GTG GAG ATG GCG CTG GAG GAC GTG AAT AGC CGC AGG GAC ATC	624
	Pro Ala Val Glu Met Ala Leu Glu Asp Val Asn Ser Arg Arg Asp Ile	
	195 200 205	
45	CTG CCG GAC TAC GAG CTC AAG CTC ATC CAC CAC GAC AGC AAG TGT GAC	672
	Leu Pro Asp Tyr Glu Leu Lys Leu Ile His His Asp Ser Lys Cys Asp	
	210 215 220	
50	CCA GGC CAA GCT ACC AAG TAC CTG TAT GAA CTG CTC TAC AAC GAC CCC	720
	Pro Gly Gln Ala Thr Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn Asp Pro	

	225		230		235		240	
	ATC AAG ATC ATC CTC ATG CCT GGC TGC AGC TCT GTC TCC ACG CTT GTG							768
	Ile Lys Ile Ile Leu Met Pro Gly Cys Ser Ser Val Ser Thr Leu Val							
5		245		250		255		
	GCT GAG GCT GCC AGG ATG TGG AAC CTC ATT GTG CTC TCC TAT GGT TCC							816
	Ala Glu Ala Ala Arg Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser							
		260		265		270		
10								
	AGC TCA CCA GCT CTG TCC AAC CGG CAG CGC TTT CCT ACC TTC TTC CGA							864
	Ser Ser Pro Ala Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg							
		275		280		285		
15								
	ACT CAT CCC TCG GCC ACG CTC CAC AAC CCT ACG CGA GTG AAG CTC TTT							912
	Thr His Pro Ser Ala Thr Leu His Asn Pro Thr Arg Val Lys Leu Phe							
		290		295		300		
	GAG AAG TGG GGC TGG AGG AAG ATT GCC ACC ATC CAG CAG ACC ACC GAG							960
20	Glu Lys Trp Gly Trp Arg Lys Ile Ala Thr Ile Gln Gln Thr Thr Glu							
		305		310		315		320
	GTG TTC ACA TCG ACT CTG GAC GAC CTA GAG GAA CGA GTG AAG GAG GCT							1008
	Val Phe Thr Ser Thr Leu Asp Asp Leu Glu Glu Arg Val Lys Glu Ala							
25		325		330		335		
	GGG ATT GAG ATT ACT TTC CGC CAG AGC TTC TTC TCA GAT CCT GCC GTG							1056
	Gly Ile Glu Ile Thr Phe Arg Gln Ser Phe Phe Ser Asp Pro Ala Val							
		340		345		350		
30								
	CCT GTC AAG AAC CTC AAG CGC CAG GAT GCC CGA ATC ATC GTG GGA CTT							1104
	Pro Val Lys Asn Leu Lys Arg Gln Asp Ala Arg Ile Ile Val Gly Leu							
		355		360		365		
35								
	TTC TAT GAG ACT GAA GCC CGG AAA GTG TTC TGT GAG GTA TAC AAG GAG							1152
	Phe Tyr Glu Thr Glu Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu							
		370		375		380		
	CGG CTC TTT GGG AAG AAG TAT GTG TGG TTC CTC ATT GGG TGG TAT GCT							1200
40	Arg Leu Phe Gly Lys Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala							
		385		390		395		400
	GAC AAT TGG TTC AAG ACC TAC GAC CCC TCC ATC AAC TGC ACA GTG GAT							1248

SUBSTITUTE SHEET (RULE 26)

ACT CCC AGC CCA ACT TGA

1746

Thr Pro Ser Pro Thr *

580

5

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 581 amino acids

10 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

Met Leu Leu Leu Leu Leu Pro Leu Ala Leu Ala Pro Leu Phe Leu Arg
 1 5 10 15

20

Pro Pro Gly Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly
 20 25 30

25

Cys Gln Ile Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly
 35 40 45

Leu Thr Arg Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr
 50 55 60

30

Glu Ile Glu Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys
 65 70 75 80

Val Arg Lys Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro
 85 90 95

35

Ser Arg Cys Val Arg Ile Cys Ser Lys Ser Tyr Leu Ala Leu Glu Asn
 100 105 110

40

Gly Lys Val Phe Leu Thr Gly Gly Asp Leu Pro Ala Leu Asp Gly Ala
 115 120 125

Arg Val Asp Phe Arg Cys Asp Pro Asp Phe His Leu Val Gly Ser Ser
 130 135 140

Arg Ser Ile Cys Ser Gln Gly Gln Trp Ser Thr Pro Lys Pro His Cys
 145 150 155 160

5 Gln Val Ser Arg Thr Pro His Ser Glu Arg Arg Ala Val Tyr Ile Gly
 165 170 175

Ala Leu Phe Pro Met Ser Gly Gly Trp Pro Gly Gly Gln Ala Cys Gln
 180 185 190

10 Pro Ala Val Glu Met Ala Leu Glu Asp Val Asn Ser Arg Arg Asp Ile
 195 200 205

Leu Pro Asp Tyr Glu Leu Lys Leu Ile His His Asp Ser Lys Cys Asp
 15 210 215 220

Pro Gly Gln Ala Thr Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn Asp Pro
 225 230 235 240

20 Ile Lys Ile Ile Leu Met Pro Gly Cys Ser Ser Val Ser Thr Leu Val
 245 250 255

Ala Glu Ala Ala Arg Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser
 260 265 270

25 Ser Ser Pro Ala Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg
 275 280 285

Thr His Pro Ser Ala Thr Leu His Asn Pro Thr Arg Val Lys Leu Phe
 30 290 295 300

Glu Lys Trp Gly Trp Arg Lys Ile Ala Thr Ile Gln Gln Thr Thr Glu
 305 310 315 320

35 Val Phe Thr Ser Thr Leu Asp Asp Leu Glu Glu Arg Val Lys Glu Ala
 325 330 335

Gly Ile Glu Ile Thr Phe Arg Gln Ser Phe Phe Ser Asp Pro Ala Val
 340 345 350

40 Pro Val Lys Asn Leu Lys Arg Gln Asp Ala Arg Ile Ile Val Gly Leu
 355 360 365

Phe Tyr Glu Thr Glu Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu
 370 375 380

Arg Leu Phe Gly Lys Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala
 5 385 390 395 400

Asp Asn Trp Phe Lys Thr Tyr Asp Pro Ser Ile Asn Cys Thr Val Asp
 405 410 415

10 Glu Met Thr Glu Ala Val Glu Gly His Ile Thr Thr Glu Ile Val Met
 420 425 430

Leu Asn Pro Ala Asn Thr Arg Ser Ile Ser Asn Met Thr Ser Gln Glu
 435 440 445

15 Phe Val Glu Lys Leu Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr
 450 455 460

Gly Gly Phe Gln Glu Ala Pro Leu Ala Tyr Asp Ala Ile Trp Ala Leu
 20 465 470 475 480

Ala Leu Ala Leu Asn Lys Thr Ser Gly Gly Ser Gly Arg Ser Gly Val
 485 490 495

25 Arg Leu Glu Asp Phe Asn Tyr Asn Asn Gln Thr Ile Thr Asp Gln Ile
 500 505 510

Tyr Arg Ala Met Asn Ser Ser Ser Phe Glu Gly Val Ser Gly His Val
 515 520 525

30 Val Phe Asp Ala Ser Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln
 530 535 540

Leu Gln Gly Gly Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys
 35 545 550 555 560

Asp Asp Leu Ser Trp Ser Lys Thr Asp Lys Trp Ile Val Thr Ser Arg
 565 570 575

40 Thr Pro Ser Pro Thr
 580

((2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 16862 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

15 (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

- 20 (A) NAME/KEY: exon
(B) LOCATION:3415..3440

(ix) FEATURE:

- (A) NAME/KEY: intron
(B) LOCATION:3441..3903

25

(ix) FEATURE:

- (A) NAME/KEY: exon
(B) LOCATION:3904..3988

30

(ix) FEATURE:

- (A) NAME/KEY: intron
(B) LOCATION:3989..4689

(ix) FEATURE:

- 35 (A) NAME/KEY: exon
(B) LOCATION:4690..4893

(ix) FEATURE:

- 40 (A) NAME/KEY: intron
(B) LOCATION:4894..5645

(ix) FEATURE:

- (A) NAME/KEY: exon

(B) LOCATION:5646..5831

(ix) FEATURE:

(A) NAME/KEY: intron

5

(B) LOCATION:5832..7181

(ix) FEATURE:

(A) NAME/KEY: exon

10

(B) LOCATION:7182..7202

(ix) FEATURE:

(A) NAME/KEY: intron

(B) LOCATION:7203..8307

15

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION:8308..8803

(ix) FEATURE:

20

(A) NAME/KEY: intron

(B) LOCATION:8804..12266

(ix) FEATURE:

25

(A) NAME/KEY: exon

(B) LOCATION:12267..12401

(ix) FEATURE:

(A) NAME/KEY: intron

(B) LOCATION:12402..12815

30

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION:12816..12986

35

(ix) FEATURE:

(A) NAME/KEY: intron

(B) LOCATION:12987..14085

(ix) FEATURE:

40

(A) NAME/KEY: exon

(B) LOCATION:14086..14187

(ix) FEATURE:

(A) NAME/KEY: intron
(B) LOCATION:14188..14473

(ix) FEATURE:

5 (A) NAME/KEY: exon
(B) LOCATION:14474..14539

(ix) FEATURE:

10 (A) NAME/KEY: intron
(B) LOCATION:14540..14998

(ix) FEATURE:

15 (A) NAME/KEY: exon
(B) LOCATION:14999..15190

(ix) FEATURE:

(A) NAME/KEY: intron
(B) LOCATION:15191..16862

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

	GATCATATTA ATTTGAAGGT GGCAGGGCAG GATGGTTCTG TGGTGCAGTT TAAGATTAAG	60
25	AGGCATACAC CACTTAGTAA ACTAATGAAA GCCTATTGTG AACGACAGGG ATTGTCAATG	120
	AGGCAGATCA GATTCCGATT CGACGGGCAA CCAATGAAAC AGACACACCT GCACAGTTGG	180
	AAATGGAGGA TGAAGATACA ATTGATGTGT TCCAACAGCA GACGGGAGGT GTCTACTGAA	240
30	AAGGGAACCT GCTTCTTTAC TCCAGAACTC TGTTCCTTAA AGACCAAGAT TACATTCTCA	300
	ATTAGAAAAC TGCAATTTGC TTCCACCACA TCCTGACTAC TACCGTATAG TTTTCTCTAT	360
35	TCTTTCATTT CCCCTTCCC CATTCCTTTA CTGTACATAA AGTAACTGGT ATATGTGAC	420
	AAGCATATTA CTTTTTTTTT TAAAACTAA ACAGCCAATG GTATGTTTTG ATTGACATCA	480
	AGTGGAGACG GGGGGGAAAA TACTGATTCT GTGAAAATAC CCCCTTCTC CATTAGTGGC	540
40	ATGCTCATTC AGCTCTTATC TTTATATTCC AGTAAGTTAT TTTGCTCTCA CTGTTTTAAC	600
	AACAACAACA AAAAAACAAC AACATAAAAA TCCTTGCATA CTTGTTCAA TTGGAGAATT	660

	TTAATGTTTT TCATTTATCA TTGTAAAACC AAGGACAATT TTATAACTTT TTTGTACTTA	720
	GCTGTTACAT GCAGAGCAAT CTGTCTTTAA GTAGGGATAA ATTACTCTAA AACAAAAAAG	780
5	AATCCTAGAT AGTTTTCCCT TCAAGTCAAG CGTCTTGTTG TTTAAATAAA CTTCTTGTTT	840
	AAAAAAAAAA AAAGTAAAAA AGAAAAGTTA TGCAACAATT AATGGCCCAG AGGCAATCCT	900
10	TGTTAACATT TTGATGCATC TTTTAGCTGT TTTTTTTTTT TTTTTTTTTT TTGACTGAGT	960
	TTGACTCTTG TCACCCAGGC TGAAGTGCAA TGGCATGGCA TGATCTTGGC TCACTGCAAC	1020
	CTCCGCCTCC CGGGTTCAAG TGATTCTCCT GCCTCAGCCT CCTGAGTAGC TAGGATTACG	1080
15	GGCATGCACC ACCATGCCTG GCTAATTTTG TATTTT TAGT AGAGTTGGGG CTTCTCCACA	1140
	CTGGTCAGGC TGGTCTCGAA CTCCCAACCT CAGGTGATAA GGAAGGGGC ACTATTGACA	1200
20	TTTATGGTTG GGGCAGAGGT GTAAGATATT CTTCAAAGCA CTACCTACAT GTTGAAGAAT	1260
	TGTTCCCTCAC CCAGATTCTC AAAAGTCCCC CAGGACATTC ACGTAGTGAA AACCTGTGTT	1320
	TAATTATCTG AGCCTATAAC TTAATACAGT TTTAAAATTT TTTTAAAT ATACAGTGAA	1380
25	CTTTCTAGGA ATGCAATTAT AGTTGTGTGT AAAATTAGGG AAAATTAAC TGTCTACCAA	1440
	GAGTTGTTCA ACATTTTGTT AAATCACTTC ATTGATGGCA ACATGCTGGA GGTAGTTGAG	1500
30	TCACCAACTC AGCACCTGGA TCAGCCTGTG TTGGTAGCAG TTTCATCCCC GTGGTTCTGT	1560
	GAATAGGTGG AAGCATCTGC TTACTCCATC AGGACTTCTA GGGTAGTCGG GCCTTGGCAC	1620
	TCACACATTA AAATACTGTT TATGTTATTT TATTGCAAGT TACTTTTCTT TCATTTCCCC	1680
35	TTTACGTTAC AGAAAGGGAA GCATTTTGCT TTCTGTTTAA AGTTGTGTAT GTAGGTAGGT	1740
	TATATCATCT AWGACTTTCT CTCCCTCCTT CCCTTCTTT TTGTTTGAGA TGGAGTCTTG	1800
40	CTCTGTCACC CAGGCTGGAG TGCAGTGGTG CGATCTTGGC TCACTGCAAC CTCTGCCTCC	1860
	CGGGTTCAAG CGATTCTGGT GTCTCAGCTG GGATTACAGG CGCACACCAT CACACCACGC	1920

	TAATTTTCT ATTTTATAGTA GAGATGGGGT TTCGCCATGC TGGCCAGGCC AGGCTGGTCT	1980
	CAAACCTCTG AGCTCAAGTG ATCAGTCCGC CTCGGCCTCC CAAAGTTCTG GGATTTCAGG	2040
5	CGTGAGCCTC ATCTATGAAT CTCAATTTAG GACAGTAAAA GTGTCATTAC AAAAATATTT	2100
	ATTGTAAAA AGGGTTGGAG GTTGAGAATC TCAATTCTAG TCAGTCTCTC AGTGTTTGGT	2160
	TTCTTCCTAC CATTTTTCCT CCTAGGACCA GCCAGAAAGC AGCTTTTTTTT TTGTCCCCC	2220
10	CAACAAGGAG CCCACTGTTT CCTCTCCAG CCCAACTCA GGCCTACGAA CAACAACAGC	2280
	ACTACACACA CACACACACA CACACACACA CACACACACA CACCCCTCCA CTTCAAGGTA	2340
15	TAGCCAAGAG CTTCTGGAGC CGTCAAAAAG GTCTGTACCT GCTGTCTTTA GAGCTTCCAG	2400
	TTTGCCCTTG GTCAAGAAAT ACTGTTTGCT AGGCTCTGCT GGAGTACATC AGGTAATACT	2460
	GGCTTCTAAA CCACCCTGAG GTTCTTTTCT CTTGTCTTTT TACTCCCTTC GTACTTCAAT	2520
20	TTCTCTCCTT GATGTCCCC TCCCTGTTTT GTTTTTTGCC TCCAATCCGT TCTGCGCGTT	2580
	CCCTGCAGAG CAGGCGAGTA GCAATGCTGC TGGACCATGG AGCTGCTCTA GTCTCCCAGA	2640
25	AATCTCTTCT ACACCCAACC CTTCTTGCGC TTAGGTGGTC CTCAGTCCCC CTCCCCACC	2700
	TCCTTCTGAC CCAGGCTTCT TTCTCGCCCT CCGGTCGCAG TTCTCCTGGG CATCTGCCTC	2760
	TGCTCTCTC CTCTACCCG GATCTAGGGC TGCCTTCTCT TTGTGCAGCC GTCTTTCTCC	2820
30	ACCTTCATCC CAGACTCCCT GTCTCAGCGC CAGCTCCTCT GCCTTTGGCT CGGGTTCCCT	2880
	CTCCCCACC CCAGCTTCCA GTTGTTTGGC CCGCAGGTCC CTCGGCAGTG ACCGGCGCCC	2940
35	CCCGACGAGT GCGTGTGCAC CAGGGCACCT CCCTCTCCCC CACCTCTCAG CCCCAGCGCT	3000
	CTCCACCGCC CGCCCCACCG CGCTGTGGGC GGTCCAGGGC GGGGCTGGGA TCCGGGGCGG	3060
	CTCCCGGGC TCGGGTTGTG GGAGGCGCCC TCTCCCCGGT CTTCCCTCTCT CTCCCCCGG	3120
40	CCCTGCCTTC CTTGACCC TCCTTCTTCC CTCCGCCCCG GAGCTCTCCC TGGTCCCCGG	3180
	CGCCGCTCC TTCCCTCCCG GCTCCCCGCT CCCCCTCCC GTGGCTGCCG CCGCCCCGGG	3240

	GAAGAAGAGA	CAGGGGTGGG	GTTTGGGGGA	AGCGAGAGAG	GAGGGGAGAG	ACCCTGGCCA	3300
	GGCTGGAGCC	TGGATTTCGAG	GGGAGGAGGG	ACGGGAGGAG	GAGAAAGGTG	GAGGAGAAGG	3360
5	GAGGGGGGAG	CGGGGAGGAG	CGGCCGGGCC	TGGGGCCTTG	AGGCCCGGGG	AGAGCCGGGG	3420
	AGCCGGGCCC	GCGCGCCGAG	GTAAGAGCCA	GGGCCCCGGG	TTAGCAGGGC	TCGGAGAGGG	3480
10	GGCGCGCGGC	GTGGTGGGGG	AGGGGGCAGT	GGGCGCAGGG	CCCAGCTGGG	GGAAGCGGGG	3540
	CTGGGGGAGA	GGAGGAACCG	CGGGGATGGA	ATCGGGGAGC	GCTGAGGCGG	CCGATGCCGG	3600
	GAGCGTGGGT	AAGCCAGGCT	TCTGCGAGCC	GCGGGGGCCG	GGGGAGAGGA	GGTGGTGAGA	3660
15	GGTGGAGTCC	GGGAGGGTTG	GGGGCCGAGG	GAGGCAGGAG	GAGGGTGGGG	ACAGGCTTTC	3720
	TCTCCTCCTC	TCCCCCACC	CCGCGCGGGG	CTCCGCCCCC	GCCTCCTCCG	CGGGGCGCTC	3780
20	TCTTGGTCCC	CAGGCTGAGC	CCGGTCGGAG	CCTGCGAGGC	AACCGGCAAG	AGGTCGAGTA	3840
	GTCTCCGGGT	GCGGGCCGCG	CCGGCGGGGC	TCGGTCCAGT	CCTCATGGCC	GCCTCTCACT	3900
	TAGATGTTGC	TGCTGCTGCT	ACTGGCGCCA	CTCTTCCTCC	GCCCCCGGG	CGCGGGCGGG	3960
25	GCGCAGACCC	CCAACGCCAC	CTCAGAAGGT	GCATCCTTCT	TCGACGACCT	CCGGCCCTCC	4020
	TTCGCTCCAC	TTCCCTTTCC	CTGCATCTCC	TCATTTCTGG	TCCTCATCAC	TATCCCATCA	4080
30	GTCCCACATA	TCATCCCGGT	CTGGCAACCC	CTTCTGCTCG	GCCCGACTTT	ACTACTGCTG	4140
	ACCTCCTTCT	GTCACCCAC	GTTACTATCC	AGCACCTCTT	TTCTCTGCCC	ACATTGCTAC	4200
	ACTATACCAC	CTTCCTGTGC	ATTTTCTCCG	CCTCAATCCC	CTTTCCCAGC	CCCACATTAC	4260
35	TACCTCAATT	ACTCCCTTTT	CTTGGTCCCA	CTTTGCTGTC	CAGATGATCT	TATTAGCCTC	4320
	CCTTTATCCT	CCTATCCTAA	TTCAACTGGA	ATATCCTCAT	TTAGCCTTTT	TTTTTAAAGA	4380
40	AAAGCTCCAC	CCACATATCA	TACCCTTCAT	GATTTCTTAA	TTACTTTTCT	TTCTTACCTC	4440
	CACCCAGCAC	CCTTCCCTCC	CCACTTGTGG	GTTCTCTCAT	CAGCTTTAAC	CCTGGCCCTT	4500

	TACTCTCTGT CCTTTAGCCA GGGGATCTGT ACCTGTCCCC ACTCCCACCC TCTAGTGCCC	4560
	CATCCCTCTT CCTCTGTCCC CAGCCTGCCC ACAGACCACG CCCTACTCTC CCCTTCCTCC	4620
5	CACTGGGGAG CCTGCCTTTT CCTCTTTCCC ACCATTCTCTC TCTGTATGCC TCCCCGACTC	4680
	ACCCCTTAGG TTGCCAGATC ATACACCCGC CCTGGGAAGG GGGCATCAGG TACCGGGGCC	4740
	TGACTCGGGA CCAGGTGAAG GCTATCAACT TCCTGCCAGT GGAATATGAG ATTGAGTATG	4800
10	TGTGCCGGGG GGAGCGCGAG GTGGTGGGGC CCAAGGTCCG CAAGTGCCTG GCCAACGGCT	4860
	CCTGGACAGA TATGGACACA CCCAGCCGCT GTGGTGAGTA GCCTCGGAAG CCCCTCCCCT	4920
15	CTTCAAGACT ATTCTTTTTT CTGCCGCAA CTTAGCATT CTGCTTGCAA GTCAGCACTT	4980
	TAAATCCAGT ATACCAAAT TCACAAATAC ATTTATTGAA TGACTACTAC ATAAGAGCAA	5040
	TTTTGCTCTG TGCGGTTGGA GGTAGTAGAG CTAGCAGCCT GCACAGTTCA TTTTCATCTC	5100
20	CCTTCATTAG GCCACTGATC ATTGGCCTAT AACATTGATA ATTCATCTTG TCAGTTATTC	5160
	TCTTTGAGGA TCATTAGTGG CAGATGATGA CAAAAAATT CTAAAATGAT TTCATCACAT	5220
25	TTTTGAATAC CTCTGTCACC AACCCAGAGA CCATATGCCC AAGAAACAAA AGCCAGTTTA	5280
	ATATTAATAG AAGCCAACTA TAATAAGAAA AGCAAATCTG ATTGTGCATC CAAAGTTATA	5340
	TACATCTACA TATTTCAAAG CCAGAGAACC GCCCACTGTA GCTGACTTTG AAGAGATCCC	5400
30	ATTTTGTGTG CTTATAGCCC CATCTTGGGT TCCTAAAATG GTAATTTTTT TTTTCTTTTG	5460
	GGAATGTGTG GATGCTTGCA CAGGTAAGGG AGGATTGGAA GATAGGTAGG CAAATCCTTT	5520
35	TCACATGTGA TTTTCTTTAG AGCAGGATGC TTGTGGACCC AAACCTGCAC CTGAGTCCC	5580
	TGCTCTTTAA AGGGAAAGAG CCTTCTTCAA CTCGCCTCTC TTCTTATTTT CCTATCTCTC	5640
	CACAGTCCGA ATCTGCTCCA AGTCTTATTT GACCCTGGAA AATGGGAAGG TTTTCCTGAC	5700
40	GGGTGGGGAC CTCCCAGCTC TGGACGGAGC CCGGGTGGAT TTCCGGTGTG ACCCCGACTT	5760
	CCATCTGGTG GGCAGCTCCC GGAGCATCTG TAGTCAGGGC CAGTGGAGCA CCCCCAAGCC	5820

	CCACTGCCAG GGTGAGGGGA ACAGCTGCCT GCATGCAGCT GATGAGGACG CTTGTGTGAG	5880
	GATGGGAGTG GGGTGGGAAT GGATAATGGG AAAGAATGGA GAGCTATAAA AATGTGGGGG	5940
5	AGGACACTGG AAAGGGGAGA TGAAAGTCCC TTTTTCCTCC ATCACCTGCC TCAAACCTCC	6000
	TCTTGCAGTC CCCGGTATCC TCTGTAGGTT GGGGGCTTCC TTCCTTTACC TTTTAAAAAA	6060
10	ATCTTCCTGC TCCCGATTCT TAGACCTCAC GTTTTCTCTT TTCCTTTATG AATCTCACCT	6120
	CTCTCACCTT CTTCAGGTTT AAATACTCCA ATTTTCCCTT TCTCTAAACT TAGAAATTTC	6180
	CATGCATCAC CCTCTTCTAG AATTCATCCC TCACCATTCC TTATATAATT GATTTATTGT	6240
15	AAAGACTCAG AAATAAATCA AACATTCTAC TAAGAAAAAT TGAGAAGGGG AGCTCTGGGG	6300
	GTGGAAACAT ATTAGGGTAA AAGACTTAAA ATTGGAGGCA GCATTATCAG AAGATGAAGA	6360
20	ACAACTCAGG GATGGGGTGG GAAGAAGACA GGTCCCTTTC TGKACTTCCT AGACAACCTC	6420
	CATTATTCCC TAAGGGAATC AGTGTTGTGT CTGTCTACYT TTTTTTTTTT TTTTTTGCCA	6480
	CGTAATTTTA CAAACTCTCC CTTTTCTAGG CACCCGAACT CTCTGCCATC TTCTCTCCTG	6540
25	GGATGCAGTC ATCCCATTTG TATGCCTCAT ACTTCCTCTA CCCTGGTAGA TTCTTTCAAG	6600
	ATCCTTGGGC TTTACTTTCC TCACATAACT CAGTTATTCT GCTTCTAGTT TACCATTTTA	6660
30	TTCTGGAAAT TGAGAGTCCC ATCCAGGGGT GGACTTATGA CACTACTGAA ACTTAGACTT	6720
	CAAGGTTCCCT CACCTACAGG GCCCTCTTCC TGTGCTCTAA TAATATAGAG GGCTCGATGG	6780
	ATATGTGTTC ATATGGTAAC AGGCTTTTGT AAAAATTGCA GAAATAAGAT TTTAACAGCA	6840
35	ATTGCTTAAA GCCAATTGTA TGTGTAATTT TTTTCTTAA AGACTCCCAA TTTTGTAATA	6900
	TTCAGGCACC ACAGAACCAA GATCTGCCCC AAACCTAGCT ATTGGCATTC CCGTCTCAAA	6960
40	TTCTGTTGTC CTATGAAAAA TCGAAGAAGA AAATAAGTCC TGACCCCTT ACCCCCAGAC	7020
	CCACCTTGTT CTTATCCCCA GGCACCTTCC CCTCAGAAAC GCAGGCTTCT GCTCTCCCCG	7080

	GTCTTCAGCA TGGACAGGTG TGGGAGGGGG CTGGGGATCA GGCCAGGGAA GCTGGGCGCC	7140
	AGTGGTAACT CTTCTCTGAT CCCCCTCTTT CCTGCTGCCA GTGAATCGAA CGCCACACTC	7200
5	AGGTGAGATG AGAAACCCTT ACCGCGCGCA CTGCAATGCC CTCCCCTTCA CTCTGCACCC	7260
	TCCACCCCCC TGAAATTCTG CCCTTAGGCT ACGGGGCGTC GTCCTTTCGC ACCTTCCCCA	7320
	ACCCACCCCA GTTTGCGGCC ACCCCCTTCC CTCCCTACCT GTTTCCTGCC TCCAGTCCCG	7380
10	GTTTTCCACG AGGCTGCGGT CTCTCCTTGT CCCTGCTTGG CTACACTTCC CTGGGCTCCA	7440
	CCTCCTCCCA GACTGAGCCT CGCCGGTGTC AGGCAGAGCC CAGCAGARGG CGGCAGGGTG	7500
15	CTGGGAGACC CTGAGCTCCC ACCACGTTTT CCCCTGTGGG GTTCCTTGCG ACCTTCGCTG	7560
	GAACCTTTTC CAGCCTGCTG CCTCCTAGGA TTTCACCTAA TGGACTTTCT CAGCCTGTCC	7620
	CACCCATCCC AACCCTGGCC AGGCCTCTCG CGCTCTTCCC CACATCTTTT CCTTCCGTGT	7680
20	ACCCCTTCCC TCGTCTTTTC TCAATTCCAT GTCCTGTCTC CCTTCTTAG GCTTCTGTCT	7740
	ACCCAGCCCC AGGCTCCCTT CCACGACCCC ACCACTCCCT CAAACCAGCC TCCCTTCCGT	7800
25	ACCCAACTCG TTCCCTCCAA AACCGTTTCC TCTCCCCCAC ATCCTCAGTG CTTCACTGTA	7860
	TCGACTCATA CTCCCACTTC AGACCTCAGG CGCCAGCCCC GTTTCCTCTCC CGTCCCACTC	7920
	GCATCCTTCC CTTCTTACCC TGGTTCTTCC GTGCTTCAGC CTCCCGCGGC TCCCTCCGCC	7980
30	CACCCCGCCC TCCTGGCAGC CCCCCTCCCC ATTTCTCCTC CCCTCGGGTC CCCTTAAGTG	8040
	AGATCCCTCC CTTCTCTTT CGTTCCTTTC CTCCTCGAGG TTGCATCCCC CCTCCCCCTC	8100
35	CCGCCCCCTC GACTGTCGCT CCCACCTCGG CGCTCGCTTC CCTCCCCGCC CCCTTCGTGC	8160
	CTCCCCAGCT CCCGCCCCGCC CCCCCACCCC CCGCTGCCGC GCGCCGCCCC TGACGTCAGA	8220
	GCCCCCTCCC AGCCCCACAT CTCCCTCCTG CTCCTCCTCC TCCCCTCCGT CGGTCACTCA	8280
40	GTCCGCGAGG AGAGTCCGCG GTGGCGGCGA CGGTGGCGAG AGCCGCGGGG GCCGTAGGAA	8340
	GCCAACCTTC CTGCTTCTC CGGGGCCCTC GCCCCCTCCT CCCCACAAAA TCAGGGATGG	8400

	AGGCGCCTCC	CCGGCACCCCT	CTTAGCAGCC	CTCCCCGGA	AAAGTGTC	CCCTGAGCTC	8460
	CTAACGCTCC	CCAACAGCTA	CCCCTGCCCC	CCACGCCATG	GGGCCCCGGG	CCCCTTTTGC	8520
5	CCGGGTGGGG	TGGCCACTGC	CGCTTCTGGT	TGTGATGGCG	GCAGGGGTGG	CTCCGGTGTG	8580
	GGCCTCCAC	TCCCCCATC	TCCCGCGGCC	TCACTCGCGG	GTCCCCCGC	ACCCCTCCTC	8640
10	AGAACGGCGC	GCAGTGTA	TCGGGGCACT	GTTTCCCATG	AGCGGGGGCT	GGCCAGGGGG	8700
	CCAGGCCTGC	CAGCCCGCGG	TGGAGATGGC	GCTGGAGGAC	GTGAATAGCC	GCAGGGACAT	8760
	CCTGCCGGAC	TATGAGCTCA	AGCTCATCCA	CCACGACAGC	AAGGTAGCCC	TGGACATGGG	8820
15	GGTGGGTGGG	AGGTGGGGGC	TTGCGGGSCA	GGGGGCCAAG	CAAGCCTGCA	CGCGCCCCCA	8880
	TCTGTCTGAG	TCGTCTCTGG	GATTGCGAGG	CAGACCCCTC	CCTTGTGTGA	CTGGCAGGAG	8940
20	ATGGGCTGGG	GGTGCAGGAG	CTTGGAAGA	GTGCAGGGG	CTGGAGGTCC	AAGATGAGGG	9000
	TCTAGGGGCT	CAAGATGGTT	AAGCATGCTG	CAAGGCAGAC	CCTTCTGCCC	CGCTGCGGGA	9060
	GTCTCGCAGA	AGTGTCGGGG	TTTGGAGAAA	CTGGTGGTGG	ATTTAAGGTA	TTAGGAGACA	9120
25	CTGATCCTCT	GAGGGAGTAA	ACTAACCCTG	GAATGGGTTG	GGGGTGGAGG	GAATGTCAGA	9180
	GGTGGGGAGC	TGGATTGGGG	GGTTACATTT	ACCATGGTAA	CAAGGTAAAA	TCTTGGCGTA	9240
30	GGTTGGAGCT	GGAAGGAATA	GGGACAGAAT	GAGGAAAATT	TTGAGAGACT	TGAGAGCTCT	9300
	AGTTTATTTA	TCTTAACAAA	ACAGCAAGGT	AGTGGTGAGC	CCTACCTGAC	TCCTTCTCAT	9360
	CCTTCTATT	CCAACCCTGT	TGAGCATTCC	CAGACTGTGG	GATAGATGGC	ATATGGTGAT	9420
35	TGGGGAAGGC	TAATGATCAA	GAGGTGGGCA	GAGGCACTGG	GAAAATGAAT	TGGATTGGGG	9480
	ATCCACATGG	GAACCCCCAC	AATAGCATGG	GGATGAAGAA	GAGTCAACAT	ACAAGGAGAA	9540
40	GAGAACAGAA	AAGAATGGCA	GTGGGGGAGA	GGGGCAAGGA	GGTAGCGTGG	GCATAATGAG	9600
	AGATCTTGGG	GCACCTTATG	GAACCTGGGT	CCTGACCTTC	CCTTCCCTTA	TAGCATTGTG	9660

	GCCTCTAGGA TGTGAGAAGG GAAATGGGAT GTAGGGATTA GGGAGGTGAG TTGAGGGAGA	9720
	GAGAGAAGGT AAGCAAATTT GGGTCCAGGG GTATTAGGGG ATAGCTTATA ATGAGGTTTT	9780
5	TTTTCCACC CCTCTCCCCT ACATGAATAA TTGGGGGTGC AGGGAAGGAT GTGACACAGG	9840
	GAAGGAGATT TAAGATCTCA AATTTATCTT CACTGACATG TGGCCCCAGA GACTTAAGGA	9900
	ATTGGGTTAG GGTGAAATAG AGTACACAAG GTGAGAATTT GGTGATCTTA CCAAATATCA	9960
10	ACCTTGGGGT GATCCAAGGA TTTATATTCA TTTTGTAGAAC ATCACTATAC ACCTAGAAAT	10020
	AGGTGTGTGT CTGGGATAGG TGTGTGAGGG GACAGAAGTG AGGTTGAAGG TAGGGTGCTT	10080
15	GAAGAGAAGA GAGCACAAGG ATTATCAGGA GCTTGGCAAG AGAACTTAAA ATCCTTTTTTG	10140
	ACTGTTACTT TCTCGTGGTT CTCAGCCTTC AGTGACATA AGAATCACCA GAGGAGTTTG	10200
	TTAAAAATAC AGATTCTAGC TCCTTGGTCA GGGATGAATC CCAAGTATTT ATCTGTATTT	10260
20	TTACTAATAG ACATCCTATC TTGGTGGATT CCTGAGCTGT AAGCTAACCC CAGAATGCCT	10320
	ATGGGAAGAG CAGCAGGGTA CAGGAAAATA ATTAGGTATT AGGGTACGGG AGGCAGGAAG	10380
25	AGAAGTAGAG GATCAGATCT GGTAGAGGGT CAGACTTGGG ACAGTCAGAG AGATCATTGG	10440
	TTTTGGGGAG TGGAGTGTGA AGAAAATGAC AGGGAGAGAT GGGTGCAGGC TTTATGATAG	10500
	GGGATCACAG GAGATAGGGG AGGCCTGGCT GTGAGCTCAA ACTCATCCAC CATGACAGGT	10560
30	GATTCCCTGG AGGTGGCGGG GAGCAGACGT GGGACCTGGG AGAAGGGAAC TGGAGAACAT	10620
	CAGAGGCATC AAGCGGGGTG GGATGGGAAG GCAGAAGAAC CAGAATGTGT CAATTGGAAT	10680
35	GAGTCGGTTT CCTGCCTGCA AATCCAGATC CTTGCAAGAG CAAAGAGAGG GAGGAGAACT	10740
	AAGGAAATCT ATTGGGGAGG GGGAGAGAAT CACGTGGTGG AGAGAATCTG CAGTGATGAA	10800
	TAGTGTGTGG AAGAGGGAAA CGGTTGCAAG AAAAGGTAGA TAAGAAATCA GGAAACAAAA	10860
40	TGGGGGGCAT GCCTTGCCCT GTTGATATGT ATCTTATATG TTCTTGAATG TCCTCATGK	10920
	TCCTATTAAC CCTGTCTTTA GAGAAGTGGA GGGGCACTGA GGGGCTGTGG GAGAAGCTGG	10980

GAGCAGGATC TGGAGTAATA GATGTGGGGA GAGTGCAGGA AGGTGGGTCC TGAGAATGGT 11040

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5 GCACTGCCCT TGGCCAGAGT GAGGGTAGGG TGGGCAACAG AGAATTCTCA GTGACTGCTG 11160

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10 AAATGTCAGG CCTCAGTGGG AGGTAAGCAG GCTCCAGAGT GCTTTCTTTA TTTCTTTCT 11280

ACTTATCCTC CCCTCCTGGC AACATTTTAC CCTCCTTAGT CCCCTGAGCC CCCTGTCTGT 11340

GTCCTCTCTG CCCTGGCTCC CCACTGGCTG CCATTTCTGTC TTCACATGCA TTGGGGTTCC 11400

15 AGCAGCTTCT GAAATGTCAT ATATCAGTGG GAGGGGAACA GGCAGTGGGA GACCCAAGGC 11460

TGGCTCTTCC TCCCCATTT CCCCTCCTCC CAAGCTTCTT TTTCTCTCCA GCTTTCTGCT 11520

20 TGTTTACTTT CCCTAGCTCC AAGCCTCTCT TTAAGGCACC TCTCAAATTG KCTGGTTTCT 11580

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CCACCCCCCA GTGTCTTTTT TTCTAATGGA CCTGTCAAAT GTCAGCGCCC AGCAGGAGGG 11700

25 ATGGATCACT GAGCGGGACC CCCTACTGGT CTTGTTCTCTG TTCTCTCTTT ACTTATCACT 11760

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30 GTGAGGAAGG AATTTTCATA ATATGGCTTT GAGCAAGCTA TCTGGGGATG TGGAAAGAGT 11880

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AAAGGGCTTG GTGACAGAGG GAAGGGGGAT GTCTGAGGGT GAGCTGAAAG GAGGTAAGGT 12000

35 GGTATGTTCA TTAATACCAA AGGAGGGGTG TGCAGGAGAG GTGATGGGTA AGGCTCCAGA 12060

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40 TGCCAGAAAG GAGAAGAAAA CGGTAATTAA TGATGAAAGT GAGTAATTGA GAAAGGAACT 12180

AATTTGTTCTG AGAAAGATAA GAGCAGGAAT TGCAGACAGG GGAGGGGCCC CAGGAGAGCT 12240

	TGCCCTCATC TCCTCTTGTC TTTCAGTGTG ATCCAGGCCA AGCCACCAAG TACCTATATG	12300
	AGCTGCTCTA CAACGACCCT ATCAAGATCA TCCTTATGCC TGGCTGCAGC TCTGTCTCCA	12360
5	CGCTGGTGGC TGAGGCTGCT AGGATGTGGA ACCTCATTGT GGTAAGCAGG GCTATGGGGG	12420
	TCAGAAGATG GGGTCATTCC CTTTTGAGCT CTAAGAAGG GACGATGGCG ATTGTGGGTT	12480
	TGTATTGAAA AGGAGTGTGG AGGACCTGCT ACTAAGATTC AGAGTCCTCT GCAGACCTGA	12540
10	GCTAGGCAGC CTCCTAGCAA CAGTGGCCTG ACAGTGCTGC AGCTGACCTC CTTCTTCAGA	12600
	AGGAATTGAA ATTAGATCAG TGAAAGAGCA TCCCGGTTGT GAGGGGTGTG TGGGCCTTTG	12660
15	AGAATCTCTT TTCCTTAGGC AGACCAGAGG TGGGGAGGTT TGGAGAGAGT AAGGAAGAGA	12720
	AACCCAAAGG CAGGAAGAGG GTTAAAGGAA CTCTTGGCCA CTCTTGGTGT CCTCAGTGAA	12780
	CAGACCCTGT TGCACTCACT CTCCCTGCCC CACAGCTTTC CTATGGCTCC AGCTCACCAG	12840
20	CCCTGTCAAA CCGGCAGCGT TTCCCCACTT TCTTCCGAAC GCACCCATCA GCCACACTCC	12900
	ACAACCCTAC CCGCGTGAAA CTCTTTGAAA AGTGGGGCTG GAAGAAGATT GCTACCATCC	12960
25	AGCAGACCAC TGAGGTCTTC ACTTCGGTGA GGAGGGGTTG GGCAAGGGGT AAAGGGACAT	13020
	AAGCTCAAAT TCCAGCACCA GGAGATGTGA CGTGAGAGTC ACTTTTAGGG GCAAGAACTT	13080
	GATTCTTCAT TGAAAGAGAA CGCATTCAT GTGGATTAAG TGCAGTTCTT TCTGTAGCCA	13140
30	GGGGAAAGAA TGAGTTGAGT TTTTGGGATC CTCTCTGTCT TTATGATTTT ATGATTTTTT	13200
	TCCCCTGTTT GATGCCCTGT TCCCCAGACA TATAGACCCA GAATGACTCA GTTCTGTAA	13260
35	AGTAGGTTCA ATCCAAAGTG GGGGCAAGAG ATGGGAGCGA AGATGAGATA GGAATCCAGG	13320
	AAGGCAGCAG ATTCCAGAGG CTTTCAAGGG GGGTGGTGGG TGGGTGTGAA TGGGAACAGA	13380
	GGGGATGGAG CCACTGGATT ACAGAGGAGA GAGGGAGAGG AAAGAGAGAG AGAGAGAGGA	13440
40	ATGAGGGAGA GGAGAGAGAG GGGCAGAAAG GCAGCTGCAT GGATCTGGTA GTTGGTACTA	13500
	AGAGAGAGAA GCCGACAGAC AAGGAGAGGT TGAGGGGGAA GAGGGAGATT TGGGGAGGTA	13560

	GAGAGGAAAT ACAGGCTCTA CATCTGAAGA AGGCAGTCTG CTCCCTCCCT TTTATTCTAT	13620
	TCTTTGGGTC TTCTATCCAC TGTGTTTCAGT GGCCCTTTAA TCCTCCCCCA CTTTCACTCT	13680
5	GATTCAGACC ATTCTTCTCT GATCCTTTGT CTGTCTGCCC ATTTGCCTCT TGAGGTTGAC	13740
	ATCATGCTGT CTGTCCCAGT CCTTGCCTTG TCTTTTCCTG GTTCCTTTAT GTTTCTTTAC	13800
10	CCCATCTTTG CCTTCAGTGG TAGGAGTGGG TGAATGGAGT GGCTTCCCCC ACACAGAGCC	13860
	TCAGCAGGGG CTCACCATTC ACCTTCCCAC TTGGAATCCA CATCCTAAGA CCAGATGCCT	13920
	TCCCGAACTC CTCACTTCAG GGACAGAAGC TGTGAAGGA AGGTTTCAGAA TGGCTGCTTC	13980
15	TTTGCTCTAT CTGAGTATTG CTCTGAAATC CCCAGTTAAC CTCTCTGGTC TTTATTCCCT	14040
	CATGCACCCC GTGTTTTTCC AACTTGTTTT TTATTCCCAC CCAAGACTCT GGACGACCTG	14100
20	GAGGAACGAG TGAAGGAGGC TGAATTGAG ATTACTTTCC GCCAGAGTTT CTTCTCAGAT	14160
	CCAGCTGTGC CCGTCAAAAA CCTGAAGGTC AGATGGCTGG GAGTGGTGGG CTCTGTTTAC	14220
	GGAGGGACCA AGCTGGGGGA CAGTGACTGG TTGGAGAGGA AAGCCAGGCG GGGGCAGGTT	14280
25	TTGATTCTCT GAGGCAATAG CATCTCCTGG GGAAGTTTAG CTCCATCTTC CAGTTGACGT	14340
	TTATTCACTA TACGTTGAGC GTTACCCTGC ACTAAGCACT TTGGGATGGG AAATCAAAGC	14400
30	TGTGAAGACA TCTGGCTTAG CCCCTCAGGC ATTCCCGGGC ATCCCTCAGG AGCTGTTTCT	14460
	TTCTCTGTTG TAGCGCCAGG ATGCCCCGAAT CATCGTGGGA CTTTTCTATG AGACTGAAGC	14520
	CCGGAAAGTT TTTTGTGAGG TGGAGTTGGA TCTGAAGAGG GAGGGGCACT GGGTGGGAGT	14580
35	TTCCCTTGGT TTTCTTGTGG GGCCTCCTCT TGGCATCTGT GCCTGAGTTG ATAGCATATG	14640
	ATCTGAGGTG ACGATTCATA GGATGTCTCT GTCTGTTGGC TCTGACTGCA TCCCTTGTCT	14700
40	GCACACACAT GATACTTTCT TCAGATCTCA TTTTCTACT GCTTTGTGTT TCCTGAGAAG	14760
	CCCATGAATT CCATCTGTCC TGACTGGCTG GAAAAGGCCA CTCAGAAATA CAGGGGCTGG	14820

	GGAGAACTT AGAAGGAAGA ATTGTCAGCC TTTCCTACTA TCCCCAAGAC TTGTAGATTT	14880
	CTCTTTT TAG TTCTACTGCT CTTCCCTGAT TCCAAGAGG CTAAATAGTA TCAAGTGAGA	14940
5	TAAGACAAAA ACAACAAAT GAGCAAACAA AACTCAGCC ATTCTCCTCT GTATTCAGGT	15000
	GTACAAGGAG CGTCTCTTTG GGAAGAAGTA CGTCTGGTTC CTCATTGGGT GGTATGCTGA	15060
	CAATTGGTTC AAGATCTACG ACCCTTCTAT CAACTGCACA GTGGATGAGA TGA CTGAGGC	15120
10	GGTGGAGGGC CACATCACAA CTGAGATTGT CATGCTGAAT CCTGCCAATA CCCGCAGCAT	15180
	TTCCAACATG GTGAGAGTGT GGGGACTTGC AGTCTGGCAC CTGGGAGGGT GGAGAGGACT	15240
15	GAGGGGGCCT TGCAGGGGAA AGGGTGGCAG GGAGAGGGTG CGGAATTTGG ATATAAAGGA	15300
	GAAGAGGGGG CTGTGCCCCAC CCTGAACTTG TCTGCATTAT GTTTCCTGTG GATCCTACCT	15360
	TTGCTCTGAC TTCCTTGGGT AGAGAGAGAA AAAAAAAAAA ACGATGGAGT TGTATGTTCA	15420
20	GTAGGTTTCT GATGAGTGGA AGGGCTGTTA CCATGGAGAC GAGGAGCAGT TGGTGAGAAG	15480
	TCAGGAGGAA CCGGCATTAA TGATAATATG GATGCTTGTA TACTCAAGCA CACCTTTACA	15540
25	GGAGCACTGT GTCTGGGCAG AATTGCATTT CATTTTCTTG GTGATTTATG TTAGTGTTTT	15600
	AGAGTTGCTT AATATTCAC TATGATTGAT ATGCAATTAG CTTGGATCCT GTTGCTTTTT	15660
	TTAATGATTC TTTTTTTAGA ATTTTATGTG GAGAAGGGGC TTTTGAAATC ATTTAGCCCC	15720
30	AGACAGCTGG TTAATGACAG ACTTGGAGCG AGGAGGCGCA TTCTCTGATT TGAGAGGGCT	15780
	GGGGCAGCCC TGCAGCTGAG GGGCAGAAGT GAGTGTGGGT GTGGGCACAG GGGAAGAGGC	15840
35	TTCTTTGTTG CTCAGCACTA CATTGTAAAG AGTACAGGAA TTTTGGGTAA GCTCGATACG	15900
	GCCACCTATG TGTCTGCTTA TTACACCAAG TGTGTACCTG CTTTGGAGAG CATGTTAGGG	15960
	GTGAGTTAAT GGTGTGAAAG CCCCCAAATA GCTTGATTTA AAAAGTTTTA CTAACAGTGG	16020
40	CATTTGTGTG G TACTTAGAT TCATGATTTT AGGGATTCTA ACAGCAAAAC TCTGATGTGG	16080
	ACTTATCTAC ATTTTGTAGA CCAGGAAAAT GAGACTCAGA GTGGTTTAAT GACTTGTCTC	16140

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5 TTATCTGCTA ACACTGTTTA GCTACTGGCA ATTGCTGAGC AAAGGAGAAA TAAGATTTAG 16320
GAAGTTGACT CTGGTGGTGT GTTGTGATGA AAGATCTGCT GCCACATGGA CTCTGATGAT 16380
10 ACACACTGTT TTGGGACATT CTAAATGGAC TCTATGTTTT AAGGTATGTT AGTTGAAAAA 16440
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ATAAACCTG GGAAAGTATT GGAAGTGGCT ACCAAAGCCA GAAAGACTTG TTGGTGCCCT 16560
15 GAGCCCAGGA CTTGCCAATC GTTGCTTCTG TCTTATAGCA GGGAGCTAGA GGAGGCTGAC 16620
AGAAAACAGG GATTGCGCTG GATCTAGTGG CTCACACCTG TAGTCCCCAG CACCTTGCGA 16680
20 GGCCAAGGCA GAGGATCACT GGAGCCCAGG AGTTCAAGAC CAGCCTGGGC AATATAGTGA 16740
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25 GA 16862

30

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 16707 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: intron

(B) LOCATION:1..2742

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION:2743..2985

(ix) FEATURE:

(A) NAME/KEY: intron

(B) LOCATION:2986..3613

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION:3614..3677

(ix) FEATURE:

(A) NAME/KEY: intron

(B) LOCATION:3678..5226

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION:5227..5304

(ix) FEATURE:

(A) NAME/KEY: intron

(B) LOCATION:5305..6848

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION:6849..6999

(ix) FEATURE:

(A) NAME/KEY: intron

(B) LOCATION:7000..7494

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION:7495..7627

(B) LOCATION:11370..11591

(ix) FEATURE:

(A) NAME/KEY: exon

5 (B) LOCATION:11592..11735

(ix) FEATURE:

(A) NAME/KEY: intron

10 (B) LOCATION:11736..12512

(ix) FEATURE:

(A) NAME/KEY: exon

15 (B) LOCATION:12513..13999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

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20	TGCAATGGCG CGATCTTGGC TCACAGCAAC CTCCGCCCTCC CAGGTTCAAG CCATTCTCCT	120
	GCCTCAGCCT CCGGAGTAGC TGGGATTACA GGCATGCGCC ACCACACCCG GCTAATTTTG	180
	TATTTT TAGT AGAGACAGGG TTTCTCCATG TTGCTCAGGC TGGTCTCGAA CTCCGGACCT	240
25	CAGGTGATCC ACCCGCCTCA GCCTCCCAA GTGCTGGGAT TACAGGCGTG AGCCACCGTG	300
	CCCAGCTAAT TTTTGTATTT TTCATAGAGA CAGGGTTTCA CCATGTTGGC CAGGCTGGTC	360
30	TTGAACTCCT GACCTCATGA TCTGCCCCGCC TTGACCTCCC AAAGTCCTGA GATTACAGAT	420
	GTGAGCCTCC GTGCCCAGGC CAAGTCTGGC TAATTTTAA AAAAATTTTG TAGAGTTGGG	480
	TCCTCTCTGT TTTGCCCAGT CTTGTCTCAA ACTCCTGGGC TCAAGGAATC CTCCTGCGTT	540
35	GGCCTCTGAA AATGAAAATG TTGGGATTAC AGGCGTGAGC CCCCTGTGCC TGGCTGCCTT	600
	TTTTTTTTTT TTTTTTTAAA GGCAGAGTCT CACTCCATCG CCCAGGCTGA AGTGCAGTGG	660
40	CGTGATCTCT GCTCACTGCA ACCTCTGCCT CTTGAGTTCA AGCGATTCTT CTACCTCAGC	720
	TTCCCAAGTA GCTGGGATTA CGGGAGCCCA CCAACACACC CAGCTAATTT TTGTATTTT	780

	AGTAGAGACG	GGTTTCACCA	GGTTGGCCAG	GCTGTCTGGA	ATTCCTGACC	TCAGGTGATC	840
	CACCCCTCCTT	GGCCTCCCAA	AGAGCTGGGA	TTACAAGTGT	GAGCCACTGT	GCCCAGCCTG	900
5	ACTTGTTTTT	TATAATGCCT	TTTTTTTTTT	TTTTTGAGAC	GGAGTCTTGC	TCTGTGCCCC	960
	AGGCTGGAGT	GTAGTGGCGT	CATCTCAGCT	CACTGTAACC	TCCACCTCCT	GGGTGGAAGT	1020
	GATT ² TTCTCA	CCTCAGCCCT	CAGCCTCCTG	AGTAGTTGGG	ACTGCAAGTG	CACACCACCA	1080
10	TGCCCAGCTA	ATTTTTTGTA	TTT ² TAGTAGA	GATGGGGTTT	CACCATGTTG	CCCAGCTGGT	1140
	CTTTAACTCC	TGAGCTCAGG	CAGTCTGCTT	ACCTTGGCCT	CCCAAAGTGC	TAGGATTAAA	1200
15	GGTGTGAGCC	ACTGTGCCTG	GCCTTTTTTT	TTTTTTTTTT	TTTTTTGAGC	AGTTTTAGTT	1260
	TCCCAGCAGA	ATTGAGATGA	AGGTACAGAA	ACTTCCCATA	TGCTTCCCAC	ATGCATAGCC	1320
	TTCTACATTA	TCGACATCCT	CCGCCAGAGT	GGTACATTTG	TTACAACTGA	TGAACCTACA	1380
20	TTGATACATC	ATAATCACCC	AAAGTCCATA	GTTTACATTA	GAGTTCACCC	TTGGTGTTAT	1440
	ATATTCTATG	GGTTTGGACA	AATGTATAAT	GAGACGTATC	TACTATTAAA	TACTTTACAG	1500
25	AGTATTTTCA	CTGGCCTAAT	CCAATGGACA	TTTATTGTTA	CTTCATTATG	GTTGGGCACA	1560
	GTGCTAGATG	CTGATGATTA	AGAGAGGGCA	TGGGATTTGG	TCTTGTCCCTC	AAGGGTAGAA	1620
	CCTAGGCCCA	TTGCATCTTC	AAAGCCCAGG	CTCCTTCAAA	GCCCAGTGTA	GTAGCAACTG	1680
30	CTGTACCTTG	CCTGTGCCCT	TTGCGTATCT	CACTCCTCTA	TCTCTCTAGA	AAGTTGGAGA	1740
	GAAAAGTGAG	CAAGGCATGA	GGAACAAAGT	TATTTATTTA	TTCTTCATTC	ATCTATTTAT	1800
35	TCTTTCATTA	CCGTTTGTGT	TAAAACATTC	CAAACCCAAA	CAATTATTTG	TATGGTCGCC	1860
	TGTGTATTAC	TTGTGGTTTC	CCAAGAAGTA	GTTGCTAAGC	TTTTCCTTGT	ATGGTTTCTG	1920
	TGAGGTAAGG	AAGGAATGAT	GTGATTTTCT	CCAGTATGTA	GAATGCAGTT	CCAAGAGGTT	1980
40	AAGTAATTTA	CTTACAGTTA	TTTAGCCAAA	CAAGGTTACT	GCAAGGTATA	TGAAGTCAGG	2040
	TCTCTTGACC	CAGTTCATGA	GAGAGTTAAA	GGAACATCA	TTCTTTT ² TAG	CTTTCATGGA	2100

	AAAAGAAGGT	TGAGTGTGG	GAGGGGTGTG	GGTAGGATTG	ATAATGGACT	TCAAAAATGT	2160
	GAAGGGTATT	TCTGTAGTTT	TCATTCTTCT	GAAAGCCTTC	TAAGAGGCAG	TGAACCAAAA	2220
5	GCACACAAGA	ATGGCAAGAA	GTTAGCATGC	TGAAGAAATA	TCCTCCTGGC	TGGCAAGCAG	2280
	AGTGAGAAGA	CTGCTATCAC	CTTTTCTAGA	ATCTTTTGGA	ATTGTAGGAG	CTGTTAGATC	2340
10	CTGGGTAAAC	TCTATGAAGA	AAGTCAGAAG	GATCAGAGAA	CATCAGTGTC	ACAGCTCTTC	2400
	ATTGGAATAT	CCATGTCTCC	TCCTTTACTC	TGCTCTACCT	TCCATCCTTT	GCCACTAATT	2460
	ATCCAGAGTG	TTTGTCAAAA	TTCTCTGTTT	GCAGTTCTGA	GCTAGCAACT	GTACACACTA	2520
15	ACACCATCAG	ACACAGCTAA	TACCTACTCT	AGTCTAGTAG	CTTCCGATCT	AAGGCAGACA	2580
	CATGGGTATA	GTAAAGATT	TTGAATGTAC	ATGTGTCCAA	TCTGACAACA	GTAACACAAA	2640
20	CCATCCATTC	AAGTAGAAGT	GATTGAGTCA	GAATTGGATT	GCACCCCTTC	CCCCACACCC	2700
	ACACACATTT	CAGTTCTTTC	CTCATGATTT	TTTCCTCCCA	AGACATCCCA	GGAATTTGTG	2760
	GAGAACTAA	CCAAGCGACT	GAAAAGACAC	CCTGAGGAGA	CAGGAGGCTT	CCAGGAGGCA	2820
25	CCGCTGGCCT	ATGATGCCAT	CTGGGCCTTG	GCACTGGCCC	TGAACAAGAC	ATCTGGAGGA	2880
	GGCGGCCGTT	CTGGTGTGCG	CCTGGAGGAC	TTCAACTACA	ACAACCAGAC	CATTACCGAC	2940
30	CAAATCTACC	GGGCAATGAA	CTCTTCGTCC	TTTGAGGGTG	TCTCTGTGAG	TTAAAACTTC	3000
	CTTCATACTC	CCCTGTCTTC	CCAATCTTGA	GAGAGACTCC	CAAGAGGCAC	CTTCTACAAA	3060
	CATGCATTCT	CTGTTTTTCT	CAGTTACTTC	TTTGCAGAAT	CAGTCTCCGA	CCAGAGAAGT	3120
35	AGGGACCTTC	AAATTAGAAG	AACCCATCAA	AGACTAGAGG	AAAAAAAATG	ATGTATTCCA	3180
	TTTTTTTTAAA	CCCCTCCCCT	CATTTCTTTT	CAAAC TAGAC	CAAGTATTCA	TGAGTCAGAT	3240
40	GAGAACTATA	GGATTTTGAA	AGACAAAACA	GTCTGAAAGG	TCATCTTCTT	ATTCCTTTTA	3300
	AAATGAAAAG	ATTAGTTTCC	AGAGAGATTT	GCTGACTTGC	TTAGGCCACA	CAACCAGAAG	3360

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	TCCAAAGAAT	AATGTTTCTA	AAATCTAGGG	TATGGGCATC	TGGGGTATGT	CCTATATGCA	3480
5	GGCAAATGCC	ATAAATAGCA	TTCATTGAGA	GGCTCAATTA	CATCAAAAAC	AGAAGGATTT	3540
	AAAGAGTCCC	TGATGTTCTC	TTTCACTCTT	GCTTTTGTCT	CCTTTGCCTT	GCTCCACATG	3600
	TTCTTTCCCT	CAGGGCCATG	TGGTGTTTGA	TGCCAGCGGC	TCTCGGATGG	CATGGACGCT	3660
10	TATCGAGCAG	CTTCAGGGTT	AGTACAGGGG	CAGGAGGGGA	CCGGACATGG	GGGCTAGGCT	3720
	GGGGCTGGGC	TGGGATGCCC	CCTGGGGAAG	AATGCCAGAG	ACATCACAAG	ATTGCCCTGG	3780
15	CACCTCCCAA	CTTCTGCCCT	TCTCTTTTAA	CTCTGTTTAT	CAAGCTTGTA	AATAATAATA	3840
	ATAATAAGCT	TAACTACAAG	AAGATTGATG	TCTTTGAGTT	GCACTGGTTT	TGCTCTTGAA	3900
	AAGAGGTGTG	CAGGCTGGGT	GTGGTGGCTC	ACCCCTGTAA	TCCCAGCACT	TTTGGGAGGC	3960
20	CAAGGCAGGC	AGATCATGAT	CATGGTCAGG	AGTTTGAGAC	CAGCCAGACC	AACATGGTGA	4020
	AACCTGTCTC	TACCAAAAAT	ACAAAAAATA	AAAAAAAAT	TAGCTGGGTG	TGGTGGCAGG	4080
25	TGCCTGTAGT	CCCAGCTACT	TGGGAGGCTG	AGGCAGGAGA	ATCACTTGAA	CCCAGGAGGC	4140
	AGAGGTTGCA	GTGAGCTGAG	ATCACGCCAC	TGCACTCCAG	CCTGGGTGAT	AGAGTAAGAC	4200
	TCTGTCTCAA	AGAAAAAAGA	AAAGAAAAGA	GACATGCAAA	TTAAAAACAG	CTACTCTCTT	4260
30	TCCCAGTGGC	TTCCATTAAT	TTCAGGAATT	TCCCCTTGAG	TGGCTTGGGT	TGAGAGGTTG	4320
	ATGACCTGTC	AGTTAGACTC	AAGAAAGCTG	AATCTAGGAG	AACCGCTATT	TTTTTTTTTAA	4380
35	GGGAATCTGC	CAAATTTTCT	TGCTGTGTAA	AGCTTCAATG	TGTATAGCTT	GGCTTTTGTG	4440
	GATTGTATTT	TCTTGAAACT	TAGCACACAG	GTATTTGCAG	AACTTCTAGG	AGTTAATTTT	4500
	TCTGCTCCAC	TCGGCTCTCA	GTCTTTTACG	GCATGGCCAA	GAGAGCTATT	TCTTGGCCTC	4560
40	CTGTGAAAAG	TTTCTTTCTT	CCTTTCTCCC	CACCTCCACA	TCCTTTCAGC	TCCTCTTTGT	4620
	ATCCAGGACA	AGAGGAAATG	GACTTCAGCC	ATGGTGAAAG	GAGTGTGAGT	TGGCTTTTGA	4680

	AGGAAAAGTT	ATGGTAACGG	AAACAGTTCT	AGAACAGAAA	TCTTAGAAAT	GACCAAATTT	4740
	TACTCAATGG	CGCTTTAAGA	GGCAGATATA	ACTTATCCAA	GGAATTAAAA	CCCAAGCCAA	4800
5	CAGAAGAGAA	TGTTCTAAAA	TTAAAAATGAA	AGCCACTGGG	AAAATAGAGC	CTGCCCATCA	4860
	TGAGAGGAAG	AATAAGCAGA	AATATGTGTA	AAGCTTTAGA	AGCCAAAATC	AAAGTGAGAG	4920
10	ACATCTCGCC	GAGAGAGGTG	TGAGGAATGG	AATAGGTGGC	AGACATGTTG	TGGAGCCTCC	4980
	TCACTGAAGA	CTTTTAAACA	TAGATATTCT	TATTTATTTG	AGTTGTCTTG	GGAACCACCT	5040
	TATATTGCTT	TTAAGTCATG	TTGCTGATTC	AAGAGTCTCG	TAGGTCCTTC	CAAGCATCCT	5100
15	TAGGGCCTCA	GGTGAAAATA	AAATCAGATA	CAACCATGCA	AAGCTCTAGG	GAAGTGGGAA	5160
	GTTGAAAATG	CCTAGGATCA	GCTCTTTGGC	TACCTGTGGT	CCTCCTTTT	ATTGTCGTCT	5220
20	GCCCAGGTGG	CAGCTACAAG	AAGATTGGCT	ACTATGACAG	CACCAAGGAT	GATCTTTTCCT	5280
	GGTCCAAAAC	AGATAAATGG	ATTGGTGAGT	GGATCTTGTT	TGTATTTTCC	TTTCTAGCCCCT	5340
	CTCGACAGTC	AAGGGAAAAA	GTCATGCCTT	TGAGTGAGGA	TGGAATGGTA	GAGACTGTTA	5400
25	GGTTGGAATG	TGGCTGGCAG	CTGGGCCAGG	AGAAAGGGTT	AAGTGAGAGT	GAATACAACC	5460
	CCTAAGGCGT	GGGTAGGGGA	GACTGGTGTA	TTTGGAGAGG	GAATAGGCGG	TGGTTAGTAC	5520
30	TATTTTTAAT	GGTGCATTGC	TGGGGTAACT	GGGGATTAGA	GGCAGGGGGT	GGGCAGAGGG	5580
	CGGGAAATGG	AAACTCCATT	TGGGTTTCCC	AGATGTCCTG	GTGTCTTGAT	ATATTTGAAC	5640
	CAGCTACTTC	AAGCCCAGAG	CTGTCTCTTT	GTCTGTCTCT	GTCAGGAAAA	CGGTTGCTTA	5700
35	AACTATGGAG	GAGGAGGGAA	AACCTCATGT	AATTGTCATC	TGCCAAAATG	TGCTTTTTAT	5760
	TTTTATATGT	ATTTTTAAAA	ATTTTCCTAT	TTTTATGTAA	TTTAGAGGTA	GACGTGCAGT	5820
40	TGTGTTACAT	GAATATATTG	CATAGTGGTG	AAGTCCGGGC	GTTTAGTGTG	CCTGTCACCC	5880
	GAACAGTGCA	CCTTGTACCT	AATAGGTAGT	ATTACATCCC	TCAAAATATA	CTTTTTTAAAG	5940

	AGAGAAAGCA AGCAGTTATT CTTTGTGTAC TTGGTCTAAA TGATAGGACA TAGGAGAGAA	6000
	ACTGAAGGTG GACAAAAGGA AGGACCTACT GATAAAAGAA AGCCTCCTTG AGAATGAAGG	6060
5	GGAGGCTCAA CCATTGAAGA TGGCTGCCGT CTGCCCTGCC CAGCAGATAT CCAGTCATTC	6120
	CCAGCACTGC TGGAGTTTTG CCCTTTTTTTT TTTTTTTTTT CAATTCGAAT TTAGGACAAT	6180
	GTTCTGGATT GCTATAAATG CTGCATGGCC TAAATTATTC TTTAAAAAAA AAAC TAAGCA	6240
10	AATTGAAATT AGTTTTTTTTT GGTGAACTCT GACAAATTG AACTTCCCCC TAATAATAAC	6300
	TGGAAAACAT ATTTGGGAAT ATTACCCTGC CAGGATTAAA ATTCAGATT AGCTTTCCTT	6360
15	CTTTTTTTGT TTGTCTTAAG AATAGGTGTC CACACTAGAT ACTTCAAGGC CTTTTTAGCT	6420
	TTATGATTCC ATAATTGTCA TTTAAACTT TGATTTGGGT TATAAGAAAC CTTATAACAT	6480
	TTTTTAATGA TCCCCTTCTT TCTCCTCCCA TTTTCCTTTG CTGTAAGAAA GACAGAAAAA	6540
20	CTTAAAGAAC AAACAAAAC AAAGACTACA ACTTTGGGGA CATGCCTCAG CATTTCCCAA	6600
	CCTATGGATA GACCATTAC TCCATCTTCT CATCTCATTT CTGGTTGCTT CCTAACGGCC	6660
25	CCAGTGGCAC TGAGCATTCT GCCTGCAGTA ACCTCTGTCC AGTGCAGTTA GGGCCTCATG	6720
	TCCCCAGCCA ATGACTGAAT GTCCATCAGC AATCTAGTTC TTTGCCCTTT TCTCCTATCC	6780
	CGTCTTCATT CTTTGTCTT CCTTCCCTTC TCTTTTCCCT TCCCCTCTTC CTCCCCTGTG	6840
30	CCATGCAGGA GGGTCCCCC CAGCTGACCA GACCCTGGTC ATCAAGACAT TCCGCTTCTT	6900
	GTCACAGAAA CTCTTTATCT CCGTCTCAGT TCTCTCCAGC CTGGGCATTG TCCTAGCTGT	6960
35	TGTCTGTCTG TCCTTTAACA TCTACAACTC ACATGTCCGG TAAGTTTCTC TTCTGACGTT	7020
	TTCTTGTCT GCCTCTCTGA GATACTGATC ATGTTCTGG ACAGGATGAG AATAAAACCT	7080
	GTGTAACCTC CATGGCCATG TATCATGGAG TTTTTCATTC TGACTTGTTG AGAATGAAAA	7140
40	CAGGGAAACC AGATATAACC CCCACTCCTA CTCAAAGTA GCTAACGGGA GGAAAAAAGA	7200
	AAAGAAGAGA AAAAAACAAC CTTTGGGGCC AGGTCTCACA GTCTTGGA CTACATAAAT	7260

	AGCCTGTATT CTAGTGGGGG CCTGTGCTTG GGAAGCCCTC TGCAACTCCA TCTTCAGCCC	7320
	CATGACTGCA TTGCTCTGCC TCTCAAGGCT CCACTGTCTT CTCCAATCCT GTCTTCCTTT	7380
5	AGCCCCCTGGC CCTGAAATTA GGGTCATGCC ATTGCGTGGT ATTTGGAGAG CTCAGCCTCC	7440
	CTGGAGAAGA GGGGTAATTC TCTCTCCCTC TCACCCTCTC CACCTCTGCC CTAGTTATAT	7500
10	CCAGAACTCA CAGCCCAACC TGAACAACCT GACTGCTGTG GGCTGCTCAC TGGCTTTAGC	7560
	TGCTGTCTTC CCCCTGGGGC TCGATGGTTA CCACATTGGG AGGAACCAGT TTCCTTTCGT	7620
	CTGCCAGGTG AGGAGGTGGT GGGCAAATTC CTTACAGGAT GTGACTCTCC CACCCGTCTC	7680
15	AGGAGCACCT TCCATGATTT ATGATTCTCT GCCCTTCCTC CTCAGCTTTC CCTGACTCTT	7740
	GTCCCTGTTC TTTCTTCTA GCATCACCCC TCTGTTCTCT GTTTGGCTCT GTCCCTTCTT	7800
20	TCTGTGTCTG CAGGCCATTT TCATTCTGTA GTTTACTTGT CAGTTCCAAG GTTGCCATGG	7860
	CAGSCCTYGC AGAGAAGAGG AGGGAGCCAT TGAAGGCAAA GGAAGGGGAT CTGCTCAAAG	7920
	GTCTCCTGAA CAATGGTGGC TTGTCTGTGG TATGGGGGCT GAGAATCAGA ACTGTGGACT	7980
25	TTTTTTGGGA GCCTTTGTTG GGTTTGGAAG GATAGAAGCA GAGATGGAAA CACAGCAGAG	8040
	AGTTGGGGGG AAGGGACCAC TGCCACACAG GGGAGGAGGG GCTCTGGGAC TGTTGGTACA	8100
30	TGGAAGGTTT TAGTGCTGTG GGGAGAGGCC AGCTTCAACA GTGATAGTTG AGTGTTCTC	8160
	TTTTCCACTG GTGGAAACAC CCACTCTTTC TCCTGATCTG CCTGCCTGTC CTTGCTCTCT	8220
	CTTTTTCTCT TGCTCTGTGC TGTCTGATC ATACATCTGT GCACATGGCA TTTCCATGCA	8280
35	CATGCACATG CAGTTCATCA GGAATCCTCT GTTCCCAGTG AGGCCAGAGT GCAGCTGGAG	8340
	AAGCAGACAA TTAGCTGTAG TGCAATAGGA GAGGTTCAG AGTAGGGATC TGCACAAAGT	8400
40	GCTTTGGGGG CAAAGAAGGG AACACAGTTC ACTGCTGGCG TGATTGGGTG GACCTCACTG	8460
	AAGAGGTGGC ATTTGAATAC TGAAGGACAA ATAGGATTTT ATCAGCTAGA GAAATAGAGG	8520

	AAGGCTACTT CAGGGGCATA GGGAGCATCG TGTGGCTAGA AAATACATGA AAGAGAGTAG	8580
	ATGAAGAGAA AGTGAGTAGT TCAGCATGGC TGGAGCGTGG GGTAGGTGTG GGGCTGGGAG	8640
5	ATGAGCCTAG CTGGACAGGT GGATGGGAGC ATGTTGTGAA GGGTCTGTGT CATATCCAGA	8700
	AGTGTTTCAGG CTATAACTTA TAGATATTGG GGAGTGGTTG GAGGTTTTTG GCCACTAAAG	8760
	CCAGGAGGTT TTAGCAAGAT CACCCTGGTG GTGTGGAAGT AGAGGGTGGA TGGGAGGAAT	8820
10	TGTTCAAGGT GGGGAGACTG CTCTCCTCCT GCCGCTCCCC GTCCTGCTCA CATTTTCGCA	8880
	TCCTCCCTGT GCCACCATGA GCTCCCTGCC CGTGCTCCCT GCCCACTCTC CCTTAGGGTT	8940
15	CTGCCCATCC TTACTGCAGT CCCGGCTACT ACTCTACCCT GTTCTGCCTG TGCCCTCTCT	9000
	TCCTTTCTAG GCGCGCCTCT GGCTCCTGGG CCTGGGCTTT AGTCTGGGCT ACGGTTCCAT	9060
	GTTACCAAG ATTTGGTGGG TCCACACGGT CTTACAAAAG AAGGAAGAAA AGAAGGAGTG	9120
20	GAGGAAGGTG AGCTGCTGCC CAATCCTCAG CCCCCARATC CTTGGCTCCT GGGGCACAGA	9180
	GCATTTTCCC CTGACGTGCC TGTTCTCCCC ACATATTTAT CCAGACTCTG GAACCCTGGA	9240
25	AGCTGTATGC CACAGTGGGC CTGCTGGTGG GCATGGATGT CCTCACTCTC GCCATCTGGC	9300
	AGATCGTGGA CCCTCTGCAC CGGACCATTG AGGTACCACT GGAGAGGAGG TGCTATGGTC	9360
	AGGAGAATGA GCAGGGCTCA GTGGCCATCA GGGCCCTGGG GCTGTGTGTG TCTTGAGGGA	9420
30	TGAAGCTACT TGGAGAGAGT GCCTTCCTCG TATTGGAAGC TCTTCCTTTC CTTCTAGAA	9480
	GGAGCCCCTC ATAGGCCTCC AGATTCAGCT GAAGAAAGGA AGGGGTGGGA ATCTGGGAAG	9540
35	GGTGTGTAGA ACTTCCAGGC ATCAGGGAAA GTGGGGAACA AGCACCTCCA AGGGTTCAGG	9600
	AAAACATTCT TAGGCCTAGA ATGAGATTTG GCATCAGCAT TGAGGGTCTC ATAGGAAAAC	9660
	AGTTGGAAGC CAGAGACTGA GAAGCGTTGA GGAGAGGAGG GGAGGCTGGC AACCATCTTT	9720
40	CTTGTGACCT TGTTTCTGCC CTAGACATTT GCCAAGGAGG AACCTAAGGA AGATATTGAC	9780
	GTCTCTATTC TGCCCCAGCT GGAGCATTGC AGCTCCAGGA AGATGAATAC ATGGCTTGGT	9840

	GTGTGGGATG TGGGCAAAGG AGGGCAGGGA TGCACAAAGG CAGGAGGGAA GGCAGGGGTA	9900
	GAGGGCTTGG AGGGAGAGGG GTCTTTGGAA GAGGAGGTAG AGAGCTTGTC AACCCAGTTT	9960
5	GAACACCCTA CTCTTTGTTA TTGCACTAAT CTTTTCTGAG AATAGGGGAG AGTTGCTCTT	10020
	TTGCTATGAG GAGCTTAGGG CCCAAAGCAC AGAAAGCACA GATGAAGAAC TTGTGTTTCTAG	10080
10	CAGAGGAACA AGTGGGGGTA ACCCCACCTC CAGACTTGAC ATTATCTTTT AGATCCCCCT	10140
	TGGCCTTATT AGCATTGTTC GATTCATGGT CACAAATTGC AAACCTACCC TCTGCCTGGA	10200
	AAGCCACCTT CCCACCTGTA GGGTAAGGGT GAGGCATGTG TGGCCCAGAC TGGCCTATTT	10260
15	CTAGATATTC AACAAGCCCT TGCCTGACTG ACAGCAGCTT GCCACCATTG CTTTCCTGTG	10320
	TGAATCCCAG GAAAAAGTGA TGTGGTCTGG GCAAGTTGGG TGGACATAAG GGATAGGGGA	10380
20	CACAGGGTGA GGTTTGCTAG GTCAGAGGGG TTGGATTGGA GAGGAGGGCC CCCTTTCCAT	10440
	TTGAGAGTAG GTGAAGGGCA GAGAGGGGAT GGGGATTGAG TGAGGAGCAT TGTGGTCTTT	10500
	GTTGCTCAAG TGACTCTCTC CTGCCATCCT AGGCATTTTC TATGGTTAAC AAGGGGCTGC	10560
25	TGCTGCTGCT GGGAATCTTC CTTGCTTATG AGACCAAGAG TGTGTCCACT GAGAAGATCA	10620
	ATGATCACCG GGCTGTGGGC ATGGCTATCT ACAATGTGGC AGTGAGCACT GACCCCATGG	10680
30	CATTGACCCT GTAGGCTGAC CACAGCAGCC CAGATATAGA GGACTAGGAA GAATCAATGC	10740
	TAGATCTGGG ATCGGTTGCT TAGAAGTCTT AAAAAGTTTG TTAATTCTTC AGGTCTATAA	10800
	AGCACTTTAC AGTTTACAAA GCTCACTACA GACATTGTAT CATTAATCTT GCAACTACCC	10860
35	AGTGAAGTAG ATATTAGTAT CCCCACTTTA TAGGTGAGGA AACAGAAACA CAGAGACGTT	10920
	AAATTGCTTG TCTGTGGTTA ATGGGCTGGA CTCTATTGAC ATTTCTTGCC AGGGACCGAC	10980
40	TCTGGAGGAC CCGGAATCTG TGCATAGAGA TCCTGGGAGT TCCTGCCTTG AGGGGAGGGG	11040
	TTAACCAAGA GTGAAAACCTG GTTTGGGACA GTTTGAGATT TTTCTCAATC TATATTGAGG	11100

	ATGATCCTGA	ATTTGGATCC	TTTTCAAAGG	GAAAGTTCAC	CAGGAAACTG	TCTGCATAGA	11160
	CTCCCTCCCA	TGGGAAGTAA	ACTCTGGATC	TTGTCTGAGC	CTGCAGACCT	GAGACTCCCT	11220
5	CAATGTGTCT	TTCCCTCTAG	GTCCTGTGCC	TCATCACTGC	TCCTGTCACC	ATGATTCTGT	11280
	CCAGCCAGCA	GGATGCAGCC	TTTGCCTTTG	CCTCTCTTGC	CATAGTTTTT	TCCTCCTATA	11340
	TCAC ³ TCTTGT	TGTGCTCTTT	GTGCCCAAGG	TAAGGATCTG	GCTTTTCTCC	CACCCTCTTT	11400
10	GTTCCCATGT	TCCCTCCATC	CCTCCTTCCT	ATATTACTGA	GTTCTCTGTC	CCTTCCGTTC	11460
	ACCTCCTCT	CACTCCTCCC	CTTGTTTTGG	GCCCAACTCT	TATCAGCATT	CCTTCCACCT	11520
15	CCAACCTTCC	ATCAGCCAGT	CACTAGTACA	GTCCTTGCTG	GGCCACCCCA	CGCCCAAACA	11580
	TTTGCCCCCA	GATGCGCAGG	CTGATCACCC	GAGGGGAATG	GCAGTCGGAG	GCGCAGGACA	11640
	CCATGAAGAC	AGGGTCATCG	ACCAACAACA	ACGAGGAGGA	GAAGTCCCGG	CTGTTGGAGA	11700
20	AGGAGAACCG	TGAACTGGAA	AAGATCATTG	CTGAGGTGCG	GGGGTGGGTG	TCAGGGTAGG	11760
	GTGTTGGAGT	GGTCCAGGAG	GCTTGCGTCT	TAGCTTGGGT	TGTCTGAAGC	CAAGCCTGAG	11820
25	ATACAGGGTC	AGATGTTCTT	GGCTCATGGA	GGGAGGGTCC	TAGGAGACAA	CCTGTAAGGA	11880
	GTGAATGGAG	CAGCATAGGG	GAGGGGAAAG	GGCTGAGCAA	GATTCTATCT	CAGGCAAAT	11940
	CCAGTGTTGG	CCTGGCAGGT	GGAAGGGCTC	TGGAGTGGGA	GCTATGTGGT	TGACTCAGCC	12000
30	TCCTTAAGGC	AAGAGGATGG	CTGTTGGCTG	TAGGTGACAA	CTGGAGAGAG	GCAGCTGTGA	12060
	GCCTCTAGTA	GTCAACACTC	ACAGCAGCTG	GGTGTAGCAT	GCAGCCCCAG	CATAAAGGAC	12120
35	CTGGGCAGGC	GTTCACTGTG	CCCCAGGCTG	TCATTAGGGG	CTGGTGCAAT	GCCAAAGAGA	12180
	GGGATGTTCC	AACTGGGTTG	ACACATCTCT	CTGATTTATT	GGAAGCTCTG	TGCACTGACT	12240
	TTTCTCTCCT	TCCCCACTTT	TTCCTTTTGT	TTTTAAATTC	TCTCTTATTT	CCCTGATCGC	12300
40	ATTTTTTCTA	TCGGTATCCT	TATGTTCTCT	GGCTTTTCTT	GTTCTGTTTT	GATTTCTCCT	12360
	TTTAATTTAT	TCTGTCCACT	TACCCTACGT	CCTCCCCCTA	CATTTTCTG	TGCCCTTCCT	12420

	CTCTTTCCCT	GTGCCCTTCC	TCTCTTTCCC	TCCTCCCCAC	TCCTTCATCA	CCTCCTCTTC	12480
	TCCTACTATC	CCAATTGTGC	TTCTTCCTCC	AGAAAGAGGA	GCGTGTCTCT	GAAGTGCGCC	12540
5	ATCAACTCCA	GTCTCGGCAG	CAGCTCCGCT	CCCGGCGCCA	CCCACCGACA	CCCCCAGAAC	12600
	CCTCTGGGGG	CCTGCCCAGG	GGACCCCCTG	AGCCCCCGA	CCGGCTTAGC	TGTGATGGGA	12660
10	GTCGAGTGCA	TTTGCTTTAT	AAGTGAGGGT	AGGGTGAGGG	AGGACAGGCC	AGTAGGGGGA	12720
	GGGAAAGGGA	GAGGGGAAGG	GCAGGGGACT	CAGGAAGCAG	GGGGTCCCCA	TCCCCAGCTG	12780
	GGAAGAACAT	GCTATCCAAT	CTCATCTCTT	GTAAATACAT	GTCCCCCTGT	GAGTTCTGGG	12840
15	CTGATTTGGG	TCTCTCATAC	CTCTGGGAAA	CAGACCTTTT	TCTCTCTTAC	TGCTTCATGT	12900
	AATTTTGTAT	CACCTCTTCA	CAATTTAGTT	CGTACCTGGC	TTGAAGCTGC	TCACTGCTCA	12960
20	CACGCTGCCT	CCTCAGCAGC	CTCACTGCAT	CTTTCTCTTC	CCATGCAACA	CCCTCTTCTA	13020
	GTTACCACGG	CAACCCCTGC	AGCTCCTCTG	CCTTTGTGCT	CTGTTCTCTGT	CCAGCAGGGG	13080
	TCTCCCAACA	AGTGCTCTTT	CCACCCCAAA	GGGGCCTCTC	CTTTTCTCCA	CTGTCATAAT	13140
25	CTCTTTCCAT	CTTACTTGCC	CTTCTATACT	TTCTCACATG	TGGCTCCCCC	TGAATTTTGC	13200
	TTCTTTGGG	AGCTCATTCT	TTTCGCCAAG	GCTCACATGC	TCCTTGCCTC	TGCTCTGTGC	13260
30	ACTCACGCTC	AGCACACATG	CATCCTCCCC	TCTCCTGCGT	GTGCCCCTG	AACATGCTCA	13320
	TGTGTACACA	CGCTTTTCCC	GTATGCTTTC	TTTATGTTCA	GTCACATGTG	CTCTCGGGTG	13380
	CCCTGCATTC	ACAGCTACGT	GTGCCCCTCT	CATGGTCATG	GGTCTGCCCT	TGAGCGTGTT	13440
35	TGGGTAGGCA	TGTGCAATTT	GTCTAGCATG	CTGAGTCATG	TCTTTCCTAT	TTGCACACGT	13500
	CCATGTTTAT	CCATGTACTT	TCCCTGTGTA	CCCTCCATGT	ACCTTGTGTA	CTTCTTCCCC	13560
40	TTAAATCATG	GTATTCTTCT	GACAGAGCCA	TATGTACCCT	ACCCTGCACA	TTGTTATGCA	13620
	CTTTTCCCCA	ATTCATGTTT	GGTGGGGCCA	TCCACACCCT	CTCCTTGTC	CAGAATCTCC	13680

ATTTCTGCTC AGATTCCCC CATCTCCATT GCATTCATGT ACTACCCTCA GTCTACACTC 13740

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5 GAAAAATAAG TGGGGGCAGG TTTGGAGAGC TGCTTCCAGT GGATAGTTGA TGAGAATCCT 13860

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GGTGTCCCTT TCACACTGTG GTGTCTCTTG GGGAAGGATC TCCCCGAATC TCAATAAACC 13980

10 AGTGAACAGT GTGACTCGGC ACCTTGCAGT CTTCTGTGA ACAGAATGGG CTTCAATCCA 14040

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15 AGGTGTTTTA TTGATCCATT GAGGGCTTAG CAGAATGAAG CAGGACATGA TTAAGTCTGA 14160

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40 GAAAAACTTT CCACTGTGAT TATCCACCTT GGACCAGTTG GACTTAATTT GAGTCTCTCT 14940

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	GCAGTTTGGG	AAATGAATAG	TTGGCATCAG	AACAGCAGCA	GGAGGCTGGG	TGTGGTGGCT	15060
	CACGCCTGTA	ATCCCAGCAC	TTTGGGAGGC	TGAGGTGGGT	GGATCACGAG	GTCAGGAGTT	15120
5	CAAGACCAGC	CTGGCCAAGA	TGGCGAAACC	CTGTCTCTAC	TAAAAATACA	AAAATTAGCT	15180
	GGGCGTGATG	GTGGGTGCCT	GTAATCTCAG	CTACTCGGGA	GGCTGAGGCA	GATAATTGCT	15240
10	TGAACCCAGG	AGATGAAGGT	TGCAGTGAGT	TTGTGCCACT	GCACTCCAGC	CTGGGCGACA	15300
	GAGTGAGACT	GTCTCAAAAA	AAAAAAAAAA	GAAAAAAAAA	AAAGAAACAA	CAGTAGCAGG	15360
	AGCTATAGAA	CAGCCCTGGG	TAGAACCTAA	AAGACCCAAA	TTATCATCTC	AAACTTGCAT	15420
15	TGCACTTAAG	TGGGCTGTAA	ATTATAAACA	AAGGGTGAAA	AGTTCTACTG	TGGCCAAAGG	15480
	TAAGCCAGAC	ACTCTGCTAG	CAGGAGTGCA	GGAGTCGAGA	GCCAAACGGT	GCGGCTAGCA	15540
20	GAGTGCCCGAG	TGCAAAGGGG	TGGGAAGGAG	TGAGATTGAG	AATATTAAAA	AGGTACTTAG	15600
	AAGAGAACTT	GTAAGATTTT	TACTGGCCAA	ATTTAAACA	TGACTGAGCA	CTATTTTTCA	15660
	TACAGGCCTC	CTACTAATAA	GAAAACAATT	TTGAGATAAC	TACTTATTTG	AGTTCACAGT	15720
25	TAATGTTCCCT	GATGATTAAG	ATCAGTTGCA	AATGTTTCATC	TGTCAATGCT	TATCTACAAT	15780
	GAGACTTCAT	GTATTCATTT	CTGAAAGTGT	CTTTTCAGGG	TGAATGGTGC	TATTGATTAG	15840
30	CACTAATACT	AATTATTAGT	ACATTATATA	TAATTACAAT	GAGATATACA	CACACATACA	15900
	CACACACATA	TATACATATA	CACACACACA	ATGATATATA	ATTAATATAT	AATTGTACCC	15960
	CAAGGGGTGC	AAAGGAGATG	TGTTGCCAGG	TGGAGAGGCT	ACCGCTTGGC	AGTTCTGGGA	16020
35	GGACTTGCTC	CCTGTGCACT	GTGAGGCAGG	CTTTGCCTTT	CAGACCTGCC	TTTGGGTAGG	16080
	GTTTCAGATCA	CTTTCTAACT	CTGGAATGTC	CTAGAATGTA	GACTGCCTGC	AGGCTTCCAT	16140
40	GTCCCCTGCT	TTTCCCTGAC	TTAGCCTGTT	GCCTCCCTGC	CCTCCTGTTG	GTTGTCTACC	16200
	AGTAGAGAGC	ACTTTGTGTG	CACTTGGCTG	CTACATTAGT	TAGGTGATCT	TCAACAAGTG	16260

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5 ACGAGATCAC TTAAGAGAGC AACCAGGAGT GTTGGGCATC TCACAGCCAT TAGCTCTGGT 16440
GTGAAGGACA AATCTAAAAG CAAGGGGACT GTGTGTTTCAT TTTCTGGGGT CACAAAACATA 16500
AGGAGCAAAG CCAGTATTCA AACTGCATAT ATTATTATCT ATTGCCACAA AACCTGTTAC 16560
10 CCTAAATGGC TTCAGACAAC AATAATCATT TATTATCCAT CATGGTTTTT GTGGGCTAGA 16620
AATTCAGATA GGGTACAGTG GGGAGGGTTC ACCCTGCTCC ACAGCATCTG GAAGATCTGA 16680
15 AGTCTGAGGG TTGTTGTCCA AAAGATC 16707

20 (2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

ATGCGCGCCG GCAGCCAACA TGCTGCTGCT GCTGCTGGTG CCTCTCTTCC 50

(2) INFORMATION FOR SEQ ID NO: 63:

35

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

GGTCATCCAG CGTTGAGGTG AAGAC

25

5

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

GAAGGTTGCC AGATTATACA TCCGC

25

20

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

CCACGATGAT TCGAGCATCT TGACG

25

35

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

5

CTGGTTCCTC CCAATGTG

18

(2) INFORMATION FOR SEQ ID NO: 67:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

15

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

20

CCAGTGGACT ATGAGATTGA G

21

(2) INFORMATION FOR SEQ ID NO: 68:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

30

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

35

CTGGTTCCTC CCAATGTG

18

(2) INFORMATION FOR SEQ ID NO: 69:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

CCAGTGGACT ATGAGATTGA G

21

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2700 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..2700

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

ATG TTG CTG CTG CTG CTA CTG GCG CCA CTC TTC CTC CGC CCC CCG GGC 48

35 Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly -

1

5

10

15

GCG GGC GGG GCG CAG ACC CCC AAC GCC ACC TCA GAA GGT TGC CAG ATC 96

Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile

40

20

25

30

ATA CAC CCG CCC TGG GAA GGG GGC ATC AGG TAC CGG GGC CTG ACT CGG 144

Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg

	35	40	45	
	GAC CAG GTG AAG GCT ATC AAC TTC CTG CCA GTG GAC TAT GAG ATT GAG	192		
	Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu			
5	50	55	60	
	TAT GTG TGC CGG GGG GAG CGC GAG GTG GTG GGG CCC AAG GTC CGC AAG	240		
	Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys			
	65	70	75	80
10				
	TGC CTG GCC AAC GGC TCC TGG ACA GAT ATG GAC ACA CCC AGC CGC TGT	288		
	Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys			
	85	90	95	
15				
	GTG AAT CGA ACG CCA CAC TCA GAA CGG CGC GCA GTG TAC ATC GGG GCA	336		
	Val Asn Arg Thr Pro His Ser Glu Arg Arg Ala Val Tyr Ile Gly Ala			
	100	105	110	
	CTG TTT CCC ATG AGC GGG GGC TGG CCA GGG GGC CAG GCC TGC CAG CCC	384		
20	Leu Phe Pro Met Ser Gly Gly Trp Pro Gly Gly Gln Ala Cys Gln Pro			
	115	120	125	
	GCG GTG GAG ATG GCG CTG GAG GAC GTG AAT AGC CGC AGG GAC ATC CTG	432		
	Ala Val Glu Met Ala Leu Glu Asp Val Asn Ser Arg Arg Asp Ile Leu			
25	130	135	140	
	CCG GAC TAT GAG CTC AAG CTC ATC CAC CAC GAC AGC AAG TGT GAT CCA	480		
	Pro Asp Tyr Glu Leu Lys Leu Ile His His Asp Ser Lys Cys Asp Pro			
	145	150	155	160
30				
	GGC CAA GCC ACC AAG TAC CTA TAT GAG CTG CTC TAC AAC GAC CCT ATC	528		
	Gly Gln Ala Thr Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn Asp Pro Ile			
	165	170	175	
35				
	AAG ATC ATC CTT ATG CCT GGC TGC AGC TCT GTC TCC ACG CTG GTG GCT	576		
	Lys Ile Ile Leu Met Pro Gly Cys Ser Ser Val Ser Thr Leu Val Ala			
	180	185	190	
	GAG GCT GCT AGG ATG TGG AAC CTC ATT GTG CTT TCC TAT GGC TCC AGC	624		
40	Glu Ala Ala Arg Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser Ser			
	195	200	205	
	TCA CCA GCC CTG TCA AAC CGG CAG CGT TTC CCC ACT TTC TTC CGA ACG	672		

	Ser	Pro	Ala	Leu	Ser	Asn	Arg	Gln	Arg	Phe	Pro	Thr	Phe	Phe	Arg	Thr	
	210						215					220					
	CAC	CCA	TCA	GCC	ACA	CTC	CAC	AAC	CCT	ACC	CGC	GTG	AAA	CTC	TTT	GAA	720
5	His	Pro	Ser	Ala	Thr	Leu	His	Asn	Pro	Thr	Arg	Val	Lys	Leu	Phe	Glu	
	225					230				235					240		
	AAG	TGG	GGC	TGG	AAG	AAG	ATT	GCT	ACC	ATC	CAG	CAG	ACC	ACT	GAG	GTC	768
10	Lys	Trp	Gly	Trp	Lys	Lys	Ile	Ala	Thr	Ile	Gln	Gln	Thr	Thr	Glu	Val	
				245					250					255			
	TTC	ACT	TCG	ACT	CTG	GAC	GAC	CTG	GAG	GAA	CGA	GTG	AAG	GAG	GCT	GGA	816
	Phe	Thr	Ser	Thr	Leu	Asp	Asp	Leu	Glu	Glu	Arg	Val	Lys	Glu	Ala	Gly	
				260					265					270			
15	ATT	GAG	ATT	ACT	TTC	CGC	CAG	AGT	TTC	TTC	TCA	GAT	CCA	GCT	GTG	CCC	864
	Ile	Glu	Ile	Thr	Phe	Arg	Gln	Ser	Phe	Phe	Ser	Asp	Pro	Ala	Val	Pro	
		275					280						285				
20	GTC	AAA	AAC	CTG	AAG	CGC	CAG	GAT	GCC	CGA	ATC	ATC	GTG	GGA	CTT	TTC	912
	Val	Lys	Asn	Leu	Lys	Arg	Gln	Asp	Ala	Arg	Ile	Ile	Val	Gly	Leu	Phe	
		290					295					300					
	TAT	GAG	ACT	GAA	GCC	CGG	AAA	GTT	TTT	TGT	GAG	GTG	TAC	AAG	GAG	CGT	960
25	Tyr	Glu	Thr	Glu	Ala	Arg	Lys	Val	Phe	Cys	Glu	Val	Tyr	Lys	Glu	Arg	
	305					310				315					320		
	CTC	TTT	GGG	AAG	AAG	TAC	GTC	TGG	TTC	CTC	ATT	GGG	TGG	TAT	GCT	GAC	1008
30	Leu	Phe	Gly	Lys	Lys	Tyr	Val	Trp	Phe	Leu	Ile	Gly	Trp	Tyr	Ala	Asp	
				325					330					335			
	AAT	TGG	TTC	AAG	ATC	TAC	GAC	CCT	TCT	ATC	AAC	TGC	ACA	GTG	GAT	GAG	1056
	Asn	Trp	Phe	Lys	Ile	Tyr	Asp	Pro	Ser	Ile	Asn	Cys	Thr	Val	Asp	Glu	
				340					345					350			
35	ATG	ACT	GAG	GCG	GTG	GAG	GGC	CAC	ATC	ACA	ACT	GAG	ATT	GTC	ATG	CTG	1104
	Met	Thr	Glu	Ala	Val	Glu	Gly	His	Ile	Thr	Thr	Glu	Ile	Val	Met	Leu	
		355					360					365					
40	AAT	CCT	GCC	AAT	ACC	CGC	AGC	ATT	TCC	AAC	ATG	ACA	TCC	CAG	GAA	TTT	1152
	Asn	Pro	Ala	Asn	Thr	Arg	Ser	Ile	Ser	Asn	Met	Thr	Ser	Gln	Glu	Phe	
		370					375				380						

	GTG GAG AAA CTA ACC AAG CGA CTG AAA AGA CAC CCT GAG GAG ACA GGA	1200
	Val Glu Lys Leu Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr Gly	
	385 390 395 400	
5	GGC TTC CAG GAG GCA CCG CTG GCC TAT GAT GCC ATC TGG GCC TTG GCA	1248
	Gly Phe Gln Glu Ala Pro Leu Ala Tyr Asp Ala Ile Trp Ala Leu Ala	
	405 410 415	
10	CTG GCC CTG AAC AAG ACA TCT GGA GGA GGC GGC CGT TCT GGT GTG CGC	1296
	Leu Ala Leu Asn Lys Thr Ser Gly Gly Gly Arg Ser Gly Val Arg	
	420 425 430	
15	CTG GAG GAC TTC AAC TAC AAC AAC CAG ACC ATT ACC GAC CAA ATC TAC	1344
	Leu Glu Asp Phe Asn Tyr Asn Asn Gln Thr Ile Thr Asp Gln Ile Tyr	
	435 440 445	
20	CGG GCA ATG AAC TCT TCG TCC TTT GAG GGT GTC TCT GGC CAT GTG GTG	1392
	Arg Ala Met Asn Ser Ser Ser Phe Glu Gly Val Ser Gly His Val Val	
	450 455 460	
25	TTT GAT GCC AGC GGC TCT CGG ATG GCA TGG ACG CTT ATC GAG CAG CTT	1440
	Phe Asp Ala Ser Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln Leu	
	465 470 475 480	
30	CAG GGT GGC AGC TAC AAG AAG ATT GGC TAC TAT GAC AGC ACC AAG GAT	1488
	Gln Gly Gly Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys Asp	
	485 490 495	
35	GAT CTT TCC TGG TCC AAA ACA GAT AAA TGG ATT GGA GGG TCC CCC CCA	1536
	Asp Leu Ser Trp Ser Lys Thr Asp Lys Trp Ile Gly Gly Ser Pro Pro	
	500 505 510	
40	GCT GAC CAG ACC CTG GTC ATC AAG ACA TTC CGC TTC CTG TCA CAG AAA	1584
	Ala Asp Gln Thr Leu Val Ile Lys Thr Phe Arg Phe Leu Ser Gln Lys	
	515 520 525	
45	CTC TTT ATC TCC GTC TCA GTT CTC TCC AGC CTG GGC ATT GTC CTA GCT	1632
	Leu Phe Ile Ser Val Ser Val Leu Ser Ser Leu Gly Ile Val Leu Ala	
	530 535 540	
50	GTT GTC TGT CTG TCC TTT AAC ATC TAC AAC TCA CAT GTC CGT TAT ATC	1680
	Val Val Cys Leu Ser Phe Asn Ile Tyr Asn Ser His Val Arg Tyr Ile	
	545 550 555 560	

	CAG AAC TCA CAG CCC AAC CTG AAC AAC CTG ACT GCT GTG GGC TGC TCA	1728
	Gln Asn Ser Gln Pro Asn Leu Asn Asn Leu Thr Ala Val Gly Cys Ser	
	565 570 575	
5	CTG GCT TTA GCT GCT GTC TTC CCC CTG GGG CTC GAT GGT TAC CAC ATT	1776
	Leu Ala Leu Ala Ala Val Phe Pro Leu Gly Leu Asp Gly Tyr His Ile	
	580 585 590	
10	GGG AGG AAC CAG TTT CCT TTC GTC TGC CAG GCC CGC CTC TGG CTC CTG	1824
	Gly Arg Asn Gln Phe Pro Phe Val Cys Gln Ala Arg Leu Trp Leu Leu	
	595 600 605	
15	GGC CTG GGC TTT AGT CTG GGC TAC GGT TCC ATG TTC ACC AAG ATT TGG	1872
	Gly Leu Gly Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr Lys Ile Trp	
	610 615 620	
20	TGG GTC CAC ACG GTC TTC ACA AAG AAG GAA GAA AAG AAG GAG TGG AGG	1920
	Trp Val His Thr Val Phe Thr Lys Lys Glu Glu Lys Lys Glu Trp Arg	
	625 630 635 640	
25	AAG ACT CTG GAA CCC TGG AAG CTG TAT GCC ACA GTG GGC CTG CTG GTG	1968
	Lys Thr Leu Glu Pro Trp Lys Leu Tyr Ala Thr Val Gly Leu Leu Val	
	645 650 655	
30	GGC ATG GAT GTC CTC ACT CTC GCC ATC TGG CAG ATC GTG GAC CCT CTG	2016
	Gly Met Asp Val Leu Thr Leu Ala Ile Trp Gln Ile Val Asp Pro Leu	
	660 665 670	
35	CAC CGG ACC ATT GAG ACA TTT GCC AAG GAG GAA CCT AAG GAA GAT ATT	2064
	His Arg Thr Ile Glu Thr Phe Ala Lys Glu Glu Pro Lys Glu Asp Ile	
	675 680 685	
40	GAC GTC TCT ATT CTG CCC CAG CTG GAG CAT TGC AGC TCC AGG AAG ATG	2112
	Asp Val Ser Ile Leu Pro Gln Leu Glu His Cys Ser Ser Arg Lys Met	
	690 695 700	
45	AAT ACA TGG CTT GGC ATT TTC TAT GGT TAC AAG GGG CTG CTG CTG CTG	2160
	Asn Thr Trp Leu Gly Ile Phe Tyr Gly Tyr Lys Gly Leu Leu Leu Leu	
	705 710 715 720	
50	CTG GGA ATC TTC CTT GCT TAT GAG ACC AAG AGT GTG TCC ACT GAG AAG	2208
	Leu Gly Ile Phe Leu Ala Tyr Glu Thr Lys Ser Val Ser Thr Glu Lys	

	725	730	735	
	ATC AAT GAT CAC CGG GCT GTG GGC ATG GCT ATC TAC AAT GTG GCA GTC	2256		
	Ile Asn Asp His Arg Ala Val Gly Met Ala Ile Tyr Asn Val Ala Val			
5	740 745 750			
	CTG TGC CTC ATC ACT GCT CCT GTC ACC ATG ATT CTG TCC AGC CAG CAG	2304		
	Leu Cys Leu Ile Thr Ala Pro Val Thr Met Ile Leu Ser Ser Gln Gln			
	755 760 765			
10	GAT GCA GCC TTT GCC TTT GCC TCT CTT GCC ATA GTT TTC TCC TCC TAT	2352		
	Asp Ala Ala Phe Ala Phe Ala Ser Leu Ala Ile Val Phe Ser Ser Tyr			
	770 775 780			
15	ATC ACT CTT GTT GTG CTC TTT GTG CCC AAG ATG CGC AGG CTG ATC ACC	2400		
	Ile Thr Leu Val Val Leu Phe Val Pro Lys Met Arg Arg Leu Ile Thr			
	785 790 795 800			
	CGA GGG GAA TGG CAG TCG GAG GCG CAG GAC ACC ATG AAG ACA GGG TCA	2448		
20	Arg Gly Glu Trp Gln Ser Glu Ala Gln Asp Thr Met Lys Thr Gly Ser			
	805 810 815			
	TCG ACC AAC AAC AAC GAG GAG GAG AAG TCC CGG CTG TTG GAG AAG GAG	2496		
	Ser Thr Asn Asn Asn Glu Glu Glu Lys Ser Arg Leu Leu Glu Lys Glu			
25	820 825 830			
	AAC CGT GAA CTG GAA AAG ATC ATT GCT GAG AAA GAG GAG CGT GTC TCT	2544		
	Asn Arg Glu Leu Glu Lys Ile Ile Ala Glu Lys Glu Glu Arg Val Ser			
	835 840 845			
30	GAA CTG CGC CAT CAA CTC CAG TCT CGG CAG CAG CTC CGC TCC CGG CGC	2592		
	Glu Leu Arg His Gln Leu Gln Ser Arg Gln Gln Leu Arg Ser Arg Arg			
	850 855 860			
35	CAC CCA CCG ACA CCC CCA GAA CCC TCT GGG GGC CTG CCC AGG GGA CCC	2640		
	His Pro Pro Thr Pro Pro Glu Pro Ser Gly Gly Leu Pro Arg Gly Pro			
	865 870 875 880			
	CCT GAG CCC CCC GAC CGG CTT AGC TGT GAT GGG AGT CGA GTG CAT TTG	2688		
40	Pro Glu Pro Pro Asp Arg Leu Ser Cys Asp Gly Ser Arg Val His Leu			
	885 890 895			
	CTT TAT AAG TGA	2700		

Leu Tyr Lys *

5 (2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 899 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

15

Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly
 1 5 10 15

20

Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile
 20 25 30

Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg
 35 40 45

25

Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu
 50 55 60

Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys
 65 70 75 80

30

Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys
 85 90 95

35

Val Asn Arg Thr Pro His Ser Glu Arg Arg Ala Val Tyr Ile Gly Ala
 100 105 110

Leu Phe Pro Met Ser Gly Gly Trp Pro Gly Gly Gln Ala Cys Gln Pro
 115 120 125

40

Ala Val Glu Met Ala Leu Glu Asp Val Asn Ser Arg Arg Asp Ile Leu
 130 135 140

Pro Asp Tyr Glu Leu Lys Leu Ile His His Asp Ser Lys Cys Asp Pro

145 150 155 160
Gly Gln Ala Thr Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn Asp Pro Ile
 165 170 175
5
Lys Ile Ile Leu Met Pro Gly Cys Ser Ser Val Ser Thr Leu Val Ala
 180 185 190
Glu Ala Ala Arg Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser Ser
10 195 200 205
Ser Pro Ala Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg Thr
 210 215 220
15 His Pro Ser Ala Thr Leu His Asn Pro Thr Arg Val Lys Leu Phe Glu
225 230 235 240
Lys Trp Gly Trp Lys Lys Ile Ala Thr Ile Gln Gln Thr Thr Glu Val
 245 250 255
20 Phe Thr Ser Thr Leu Asp Asp Leu Glu Glu Arg Val Lys Glu Ala Gly
 260 265 270
Ile Glu Ile Thr Phe Arg Gln Ser Phe Phe Ser Asp Pro Ala Val Pro
25 275 280 285
Val Lys Asn Leu Lys Arg Gln Asp Ala Arg Ile Ile Val Gly Leu Phe
 290 295 300
30 Tyr Glu Thr Glu Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu Arg
305 310 315 320
Leu Phe Gly Lys Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala Asp
 325 330 335
35 Asn Trp Phe Lys Ile Tyr Asp Pro Ser Ile Asn Cys Thr Val Asp Glu
 340 345 350
Met Thr Glu Ala Val Glu Gly His Ile Thr Thr Glu Ile Val Met Leu
40 355 360 365
Asn Pro Ala Asn Thr Arg Ser Ile Ser Asn Met Thr Ser Gln Glu Phe
 370 375 380

Val Glu Lys Leu Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr Gly
 385 390 395 400

5 Gly Phe Gln Glu Ala Pro Leu Ala Tyr Asp Ala Ile Trp Ala Leu Ala
 405 410 415

Leu Ala Leu Asn Lys Thr Ser Gly Gly Gly Gly Arg Ser Gly Val Arg
 420 425 430

10 Leu Glu Asp Phe Asn Tyr Asn Asn Gln Thr Ile Thr Asp Gln Ile Tyr
 435 440 445

Arg Ala Met Asn Ser Ser Ser Phe Glu Gly Val Ser Gly His Val Val
 15 450 455 460

Phe Asp Ala Ser Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln Leu
 465 470 475 480

20 Gln Gly Gly Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys Asp
 485 490 495

Asp Leu Ser Trp Ser Lys Thr Asp Lys Trp Ile Gly Gly Ser Pro Pro
 500 505 510

25 Ala Asp Gln Thr Leu Val Ile Lys Thr Phe Arg Phe Leu Ser Gln Lys
 515 520 525

Leu Phe Ile Ser Val Ser Val Leu Ser Ser Leu Gly Ile Val Leu Ala
 30 530 535 540

Val Val Cys Leu Ser Phe Asn Ile Tyr Asn Ser His Val Arg Tyr Ile
 545 550 555 560

35 Gln Asn Ser Gln Pro Asn Leu Asn Asn Leu Thr Ala Val Gly Cys Ser
 565 570 575

Leu Ala Leu Ala Ala Val Phe Pro Leu Gly Leu Asp Gly Tyr His Ile
 580 585 590

40 Gly Arg Asn Gln Phe Pro Phe Val Cys Gln Ala Arg Leu Trp Leu Leu
 595 600 605

Gly Leu Gly Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr Lys Ile Trp
 610 615 620

Trp Val His Thr Val Phe Thr Lys Lys Glu Glu Lys Lys Glu Trp Arg
 5 625 630 635 640

Lys Thr Leu Glu Pro Trp Lys Leu Tyr Ala Thr Val Gly Leu Leu Val
 645 650 655

10 Gly Met Asp Val Leu Thr Leu Ala Ile Trp Gln Ile Val Asp Pro Leu
 660 665 670

His Arg Thr Ile Glu Thr Phe Ala Lys Glu Glu Pro Lys Glu Asp Ile
 675 680 685

15 Asp Val Ser Ile Leu Pro Gln Leu Glu His Cys Ser Ser Arg Lys Met
 690 695 700

Asn Thr Trp Leu Gly Ile Phe Tyr Gly Tyr Lys Gly Leu Leu Leu Leu
 20 705 710 715 720

Leu Gly Ile Phe Leu Ala Tyr Glu Thr Lys Ser Val Ser Thr Glu Lys
 725 730 735

25 Ile Asn Asp His Arg Ala Val Gly Met Ala Ile Tyr Asn Val Ala Val
 740 745 750

Leu Cys Leu Ile Thr Ala Pro Val Thr Met Ile Leu Ser Ser Gln Gln
 755 760 765

30 Asp Ala Ala Phe Ala Phe Ala Ser Leu Ala Ile Val Phe Ser Ser Tyr
 770 775 780

Ile Thr Leu Val Val Leu Phe Val Pro Lys Met Arg Arg Leu Ile Thr
 35 785 790 795 800

Arg Gly Glu Trp Gln Ser Glu Ala Gln Asp Thr Met Lys Thr Gly Ser
 805 810 815

40 Ser Thr Asn Asn Asn Glu Glu Glu Lys Ser Arg Leu Leu Glu Lys Glu
 820 825 830

Asn Arg Glu Leu Glu Lys Ile Ile Ala Glu Lys Glu Glu Arg Val Ser

835 840 845

Glu Leu Arg His Gln Leu Gln Ser Arg Gln Gln Leu Arg Ser Arg Arg
 850 855 860

5 His Pro Pro Thr Pro Pro Glu Pro Ser Gly Gly Leu Pro Arg Gly Pro
 865 870 875 880

Pro Glu Pro Pro Asp Arg Leu Ser Cys Asp Gly Ser Arg Val His Leu
 10 885 890 895

Leu Tyr Lys

15

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2518 base pairs
 20 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA
 25

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
 30

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION:1..294

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

ATG TTG CTG CTG CTG CTA CTG GCG CCA CTC TTC CTC CGC CCC CCG GGC 48
 Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly

40 1 5 10 15

GCG GGC GGG GCG CAG ACC CCC AAC GCC ACC TCA GAA GGT TGC CAG ATC 96
 Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile

	20	25	30	
	ATA CAC CCG CCC TGG GAA GGG GGC ATC AGG TAC CGG GGC CTG ACT CGG	144		
	Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg			
5	35	40	45	
	GAC CAG GTG AAG GCT ATC AAC TTC CTG CCA GTG GAC TAT GAG ATT GAG	192		
	Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu			
	50	55	60	
10	TAT GTG TGC CGG GGG GAG CGC GAG GTG GTG GGG CCC AAG GTC CGC AAG	240		
	Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys			
	65	70	75	80
	TGC CTG GCC AAC GGC TCC TGG ACA GAT ATG GAC ACA CCC AGC CGC TGT	288		
15	Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys			
	85	90	95	
	GTG TGA TCCAGGCCAA GCCACCAAGT ACCTATATGA GCTGCTCTAC AACGACCCTA	344		
20	Val *			
	TCAAGATCAT CCTTATGCCT GGCTGCAGCT CTGTCTCCAC GCTGGTGGCT GAGGCTGCTA	404		
	GGATGTGGAA CCTCATTTGTG CTTTCCTATG GCTCCAGCTC ACCAGCCCTG TCAAACCGGC	464		
25	AGCGTTTCCC CACTTCTTTC CGAACGCACC CATCAGCCAC ACTCCACAAC CCTACCCGCG	524		
	TGAAACTCTT TGAAAAGTGG GGCTGGAAGA AGATTGCTAC CATCCAGCAG ACCACTGAGG	584		
30	TCTTCACTTC GACTCTGGAC GACCTGGAGG AACGAGTGAA GGAGGCTGGA ATTGAGATTA	644		
	CTTTCCGCCA GAGTTTCTTC TCAGATCCAG CTGTGCCCCGT CAAAAACCTG AAGCGCCAGG	704		
35	ATGCCCCGAAT CATCGTGGGA CTTTTCTATG AGACTGAAGC CCGGAAAGTT TTTTGTGAGG	764		
	TGTACAAGGA GCGTCTCTTT GGGAAGAAGT ACGTCTGGTT CCTCATTTGGG TGGTATGCTG	824		
	ACAATTGGTT CAAGATCTAC GACCCTTCTA TCAACTGCAC AGTGGATGAG ATGACTGAGG	884		
40	CGGTGGAGGG CCACATCACA ACTGAGATTG TCATGCTGAA TCCTGCCAAT ACCCGCAGCA	944		
	TTTCCAACAT GACATCCCAG GAATTTGTGG AGAACTAAC CAAGCGACTG AAAAGACACC	1004		

	CTGAGGAGAC	AGGAGGCTTC	CAGGAGGCAC	CGCTGGCCTA	TGATGCCATC	TGGGCCTTGG	1064
	CACTGGCCCT	GAACAAGACA	TCTGGAGGAG	GCGGCCGTTT	TGGTGTGCGC	CTGGAGGACT	1124
5	TCAACTACAA	CAACCAGACC	ATTACCGACC	AAATCTACCG	GGCAATGAAC	TCTTCGTCCT	1184
	TTGAGGGTGT	CTCTGGCCAT	GTGGTGTGTT	ATGCCAGCGG	CTCTCGGATG	GCATGGACGC	1244
10	TTATCGAGCA	GCTTCAGGGT	GGCAGCTACA	AGAAGATTGG	CTACTATGAC	AGCACCAAGG	1304
	ATGATCTTTC	CTGGTCCAAA	ACAGATAAAT	GGATTGGAGG	GTCCCCCCCC	GCTGACCAGA	1364
	CCCTGGTCAT	CAAGACATTC	CGCTTCCTGT	CACAGAAACT	CTTTATCTCC	GTCTCAGTTC	1424
15	TCTCCAGCCT	GGGCATTGTC	CTAGCTGTTG	TCTGTCTGTC	CTTTAACATC	TACAACTCAC	1484
	ATGTCCGTTA	TATCCAGAAC	TCACAGCCCA	ACCTGAACAA	CCTGACTGCT	GTGGGCTGCT	1544
20	CACTGGCTTT	AGCTGCTGTC	TTCCCCCTGG	GGCTCGATGG	TTACCACATT	GGGAGGAACC	1604
	AGTTTCCTTT	CGTCTGCCAG	GCCCGCCTCT	GGCTCCTGGG	CCTGGGCTTT	AGTCTGGGCT	1664
	ACGGTTCCAT	GTTACCAAG	ATTTGGTGGG	TCCACACGGT	CTTCACAAAG	AAGGAAGAAA	1724
25	AGAAGGAGTG	GAGGAAGACT	CTGGAACCCT	GGAAGCTGTA	TGCCACAGTG	GGCCTGCTGG	1784
	TGGGCATGGA	TGTCCTCACT	CTCGCCATCT	GGCAGATCGT	GGACCCTCTG	CACCGGACCA	1844
30	TTGAGACATT	TGCCAAGGAG	GAACCTAAGG	AAGATATTGA	CGTCTCTATT	CTGCCCCAGC	1904
	TGGAGCATTG	CAGCTCCAGG	AAGATGAATA	CATGGCTTGG	CATTTTCTAT	GGTTACAAGG	1964
	GGCTGCTGCT	GCTGCTGGGA	ATCTTCCTTG	CTTATGAGAC	CAAGAGTGTG	TCCACTGAGA	2024
35	AGATCAATGA	TCACCGGGCT	GTGGGCATGG	CTATCTACAA	TGTGGCAGTC	CTGTGCCTCA	2084
	TCACTGCTCC	TGTCACCATG	ATTCTGTCCA	GCCAGCAGGA	TGCAGCCTTT	GCCTTTGCCT	2144
40	CTCTTGCCAT	AGTTTTCTCC	TCCTATATCA	CTCTTGTTGT	GCTCTTTGTG	CCCAAGATGC	2204
	GCAGGCTGAT	CACCCGAGGG	GAATGGCAGT	CGGAGGCGCA	GGACACCATG	AAGACAGGGT	2264

CATCGACCAA CAACAACGAG GAGGAGAAGT CCCGGCTGTT GGAGAAGGAG AACCGTGAAC 2324
 TGGAAAAGAT CATTGCTGAG AAAGAGGAGC GTGTCTCTGA ACTGCGCCAT CAACTCCAGT 2384
 5 CTCGGCAGCA GCTCCGCTCC CGGCGCCACC CACCGACACC CCCAGAACCC TCTGGGGGCC 2444
 TGCCCAGGGG ACCCCCTGAG CCCCCCGACC GGCTTAGCTG TGATGGGAGT CGAGTGCATT 2504
 TGCTTTATAA GTGA 2518

10

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 97 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly
 1 5 10 15
 25 Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile
 20 25 30
 Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg
 30 35 40 45
 Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu
 50 55 60
 35 Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys
 65 70 75 80
 Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys
 85 90 95
 40 Val

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 2679 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

15

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

20

(A) NAME/KEY: CDS

(B) LOCATION:1..2679

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

25	ATG TTG CTG CTG CTG CTA CTG GCG CCA CTC TTC CTC CGC CCC CCG GGC	48
	Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly	
	1 5 10 15	
	GCG GGC GGG GCG CAG ACC CCC AAC GCC ACC TCA GAA GGT TGC CAG ATC	96
30	Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile	
	20 25 30	
	ATA CAC CCG CCC TGG GAA GGG GGC ATC AGG TAC CGG GGC CTG ACT CGG	144
	Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg	
35	35 40 45	
	GAC CAG GTG AAG GCT ATC AAC TTC CTG CCA GTG GAC TAT GAG ATT GAG	192
	Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu	
	50 55 60	
40	TAT GTG TGC CGG GGG GAG CGC GAG GTG GTG GGG CCC AAG GTC CGC AAG	240
	Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys	
	65 70 75 80	

	TGC CTG GCC AAC GGC TCC TGG ACA GAT ATG GAC ACA CCC AGC CGC TGT	288
	Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys	
	85 90 95	
5	GAA CGG CGC GCA GTG TAC ATC GGG GCA CTG TTT CCC ATG AGC GGG GGC	336
	Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe Pro Met Ser Gly Gly	
	100 105 110	
10	TGG CCA GGG GGC CAG GCG TGC CAG CCC GCG GTG GAG ATG GCG CTG GAG	384
	Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val Glu Met Ala Leu Glu	
	115 120 125	
	GAC GTG AAT AGC CGC AGG GAC ATC CTG CCG GAC TAT GAG CTC AAG CTC	432
15	Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp Tyr Glu Leu Lys Leu	
	130 135 140	
	ATC CAC CAC GAC AGC AAG TGT GAT CCA GGC CAA GCC ACC AAG TAC CTA	480
	Ile His His Asp Ser Lys Cys Asp Pro Gly Gln Ala Thr Lys Tyr Leu	
20	145 150 155 160	
	TAT GAG CTG CTC TAC AAC GAC CCT ATC AAG ATC ATC CTT ATG CCT GGC	528
	Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile Ile Leu Met Pro Gly	
	165 170 175	
25	TGC AGC TCT GTC TCC ACG CTG GTG GCT GAG GCT GCT AGG ATG TGG AAC	576
	Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala Ala Arg Met Trp Asn	
	180 185 190	
30	CTC ATT GTG CTT TCC TAT GGC TCC AGC TCA CCA GCC CTG TCA AAC CGG	624
	Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro Ala Leu Ser Asn Arg	
	195 200 205	
	CAG CGT TTC CCC ACT TTC TTC CGA ACG CAC CCA TCA GCC ACA CTC CAC	672
35	Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro Ser Ala Thr Leu His	
	210 215 220	
	AAC CCT ACC CGC GTG AAA CTC TTT GAA AAG TGG GGC TGG AAG AAG ATT	720
	Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp Gly Trp Lys Lys Ile	
40	225 230 235 240	
	GCT ACC ATC CAG CAG ACC ACT GAG GTC TTC ACT TCG ACT CTG GAC GAC	768
	Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr Ser Thr Leu Asp Asp	

	245	250	255	
	CTG GAG GAA CGA GTG AAG GAG GCT GGA ATT GAG ATT ACT TTC CGC CAG			816
	Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu Ile Thr Phe Arg Gln			
5	260	265	270	
	AGT TTC TTC TCA GAT CCA GCT GTG CCC GTC AAA AAC CTG AAG CGC CAG			864
	Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys Asn Leu Lys Arg Gln			
	275	280	285	
10	GAT GCC CGA ATC ATC GTG GGA CTT TTC TAT GAG ACT GAA GCC CGG AAA			912
	Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu Thr Glu Ala Arg Lys			
	290	295	300	
15	GTT TTT TGT GAG GTG TAC AAG GAG CGT CTC TTT GGG AAG AAG TAC GTC			960
	Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe Gly Lys Lys Tyr Val			
	305	310	315	320
	TGG TTC CTC ATT GGG TGG TAT GCT GAC AAT TGG TTC AAG ATC TAC GAC			1008
20	Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp Phe Lys Ile Tyr Asp			
	325	330	335	
	CCT TCT ATC AAC TGC ACA GTG GAT GAG ATG ACT GAG GCG GTG GAG GGC			1056
	Pro Ser Ile Asn Cys Thr Val Asp Glu Met Thr Glu Ala Val Glu Gly			
25	340	345	350	
	CAC ATC ACA ACT GAG ATT GTC ATG CTG AAT CCT GCC AAT ACC CGC AGC			1104
	His Ile Thr Thr Glu Ile Val Met Leu Asn Pro Ala Asn Thr Arg Ser			
	355	360	365	
30	ATT TCC AAC ATG ACA TCC CAG GAA TTT GTG GAG AAA CTA ACC AAG CGA			1152
	Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu Lys Leu Thr Lys Arg			
	370	375	380	
35	CTG AAA AGA CAC CCT GAG GAG ACA GGA GGC TTC CAG GAG GCA CCG CTG			1200
	Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe Gln Glu Ala Pro Leu			
	385	390	395	400
	GCC TAT GAT GCC ATC TGG GCC TTG GCA CTG GCC CTG AAC AAG ACA TCT			1248
40	Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala Leu Asn Lys Thr Ser			
	405	410	415	
	GGA GGA GGC GGC CGT TCT GGT GTG CGC CTG GAG GAC TTC AAC TAC AAC			1296

	Gly	Gly	Gly	Gly	Arg	Ser	Gly	Val	Arg	Leu	Glu	Asp	Phe	Asn	Tyr	Asn	
				420					425					430			
	AAC	CAG	ACC	ATT	ACC	GAC	CAA	ATC	TAC	CGG	GCA	ATG	AAC	TCT	TCG	TCC	1344
5	Asn	Gln	Thr	Ile	Thr	Asp	Gln	Ile	Tyr	Arg	Ala	Met	Asn	Ser	Ser	Ser	
			435					440					445				
	TTT	GAG	GGT	GTC	TCT	GGC	CAT	GTG	GTG	TTT	GAT	GCC	AGC	GGC	TCT	CGG	1392
	Phe	Glu	Gly	Val	Ser	Gly	His	Val	Val	Phe	Asp	Ala	Ser	Gly	Ser	Arg	
10		450					455				460						
	ATG	GCA	TGG	ACG	CTT	ATC	GAG	CAG	CTT	CAG	GGT	GGC	AGC	TAC	AAG	AAG	1440
	Met	Ala	Trp	Thr	Leu	Ile	Glu	Gln	Leu	Gln	Gly	Gly	Ser	Tyr	Lys	Lys	
	465					470				475						480	
15																	
	ATT	GGC	TAC	TAT	GAC	AGC	ACC	AAG	GAT	GAT	CTT	TCC	TGG	TCC	AAA	ACA	1488
	Ile	Gly	Tyr	Tyr	Asp	Ser	Thr	Lys	Asp	Asp	Leu	Ser	Trp	Ser	Lys	Thr	
				485					490						495		
	GAT	AAA	TGG	ATT	GGA	GGG	TCC	CCC	CCA	GCT	GAC	CAG	ACC	CTG	GTC	ATC	1536
20	Asp	Lys	Trp	Ile	Gly	Gly	Ser	Pro	Pro	Ala	Asp	Gln	Thr	Leu	Val	Ile	
				500					505					510			
	AAG	ACA	TTC	CGC	TTC	CTG	TCA	CAG	AAA	CTC	TTT	ATC	TCC	GTC	TCA	GTT	1584
25	Lys	Thr	Phe	Arg	Phe	Leu	Ser	Gln	Lys	Leu	Phe	Ile	Ser	Val	Ser	Val	
			515					520					525				
	CTC	TCC	AGC	CTG	GGC	ATT	GTC	CTA	GCT	GTT	GTC	TGT	CTG	TCC	TTT	AAC	1632
	Leu	Ser	Ser	Leu	Gly	Ile	Val	Leu	Ala	Val	Val	Cys	Leu	Ser	Phe	Asn	
30		530					535				540						
	ATC	TAC	AAC	TCA	CAT	GTC	CGT	TAT	ATC	CAG	AAC	TCA	CAG	CCC	AAC	CTG	1680
	Ile	Tyr	Asn	Ser	His	Val	Arg	Tyr	Ile	Gln	Asn	Ser	Gln	Pro	Asn	Leu	
	545					550				555					560		
35																	
	AAC	AAC	CTG	ACT	GCT	GTG	GGC	TGC	TCA	CTG	GCT	TTA	GCT	GCT	GTC	TTC	1728
	Asn	Asn	Leu	Thr	Ala	Val	Gly	Cys	Ser	Leu	Ala	Leu	Ala	Ala	Val	Phe	
				565						570					575		
	CCC	CTG	GGG	CTC	GAT	GGT	TAC	CAC	ATT	GGG	AGG	AAC	CAG	TTT	CCT	TTC	1776
40	Pro	Leu	Gly	Leu	Asp	Gly	Tyr	His	Ile	Gly	Arg	Asn	Gln	Phe	Pro	Phe	
				580					585					590			

	GTC TGC CAG GCC CGC CTC TGG CTC CTG GGC CTG GGC TTT AGT CTG GGC	1824
	Val Cys Gln Ala Arg Leu Trp Leu Leu Gly Leu Gly Phe Ser Leu Gly	
	595 600 605	
5	TAC GGT TCC ATG TTC ACC AAG ATT TGG TGG GTC CAC ACG GTC TTC ACA	1872
	Tyr Gly Ser Met Phe Thr Lys Ile Trp Trp Val His Thr Val Phe Thr	
	610 615 620	
	AAG AAG GAA GAA AAG AAG GAG TGG AGG AAG ACT CTG GAA CCC TGG AAG	1920
10	Lys Lys Glu Glu Lys Lys Glu Trp Arg Lys Thr Leu Glu Pro Trp Lys	
	625 630 635 640	
	CTG TAT GCC ACA GTG GGC CTG CTG GTG GGC ATG GAT GTC CTC ACT CTC	1968
	Leu Tyr Ala Thr Val Gly Leu Leu Val Gly Met Asp Val Leu Thr Leu	
15	645 650 655	
	GCC ATC TGG CAG ATC GTG GAC CCT CTG CAC CGG ACC ATT GAG ACA TTT	2016
	Ala Ile Trp Gln Ile Val Asp Pro Leu His Arg Thr Ile Glu Thr Phe	
	660 665 670	
20	GCC AAG GAG GAA CCT AAG GAA GAT ATT GAC GTC TCT ATT CTG CCC CAG	2064
	Ala Lys Glu Glu Pro Lys Glu Asp Ile Asp Val Ser Ile Leu Pro Gln	
	675 680 685	
25	CTG GAG CAT TGC AGC TCC AGG AAG ATG AAT ACA TGG CTT GGC ATT TTC	2112
	Leu Glu His Cys Ser Ser Arg Lys Met Asn Thr Trp Leu Gly Ile Phe	
	690 695 700	
	TAT GGT TAC AAG GGG CTG CTG CTG CTG CTG GGA ATC TTC CTT GCT TAT	2160
30	Tyr Gly Tyr Lys Gly Leu Leu Leu Leu Leu Gly Ile Phe Leu Ala Tyr	
	705 710 715 720	
	GAG ACC AAG AGT GTG TCC ACT GAG AAG ATC AAT GAT CAC CGG GCT GTG	2208
	Glu Thr Lys Ser Val Ser Thr Glu Lys Ile Asn Asp His Arg Ala Val	
35	725 730 735	
	GGC ATG GCT ATC TAC AAT GTG GCA GTC CTG TGC CTC ATC ACT GCT CCT	2256
	Gly Met Ala Ile Tyr Asn Val Ala Val Leu Cys Leu Ile Thr Ala Pro	
	740 745 750	
40	GTC ACC ATG ATT CTG TCC AGC CAG CAG GAT GCA GCC TTT GCC TTT GCC	2304
	Val Thr Met Ile Leu Ser Ser Gln Gln Asp Ala Ala Phe Ala Phe Ala	
	755 760 765	

TCT CTT GCC ATA GTT TTC TCC TCC TAT ATC ACT CTT GTT GTG CTC TTT 2352
 Ser Leu Ala Ile Val Phe Ser Ser Tyr Ile Thr Leu Val Val Leu Phe
 770 775 780

5 GTG CCC AAG ATG CGC AGG CTG ATC ACC CGA GGG GAA TGG CAG TCG GAG 2400
 Val Pro Lys Met Arg Arg Leu Ile Thr Arg Gly Glu Trp Gln Ser Glu
 785 790 795 800

10 GCG CAG GAC ACC ATG AAG ACA GGG TCA TCG ACC AAC AAC AAC GAG GAG 2448
 Ala Gln Asp Thr Met Lys Thr Gly Ser Ser Thr Asn Asn Asn Glu Glu
 805 810 815

15 GAG AAG TCC CGG CTG TTG GAG AAG GAG AAC CGT GAA CTG GAA AAG ATC 2496
 Glu Lys Ser Arg Leu Leu Glu Lys Glu Asn Arg Glu Leu Glu Lys Ile
 820 825 830

20 ATT GCT GAG AAA GAG GAG CGT GTC TCT GAA CTG CGC CAT CAA CTC CAG 2544
 Ile Ala Glu Lys Glu Glu Arg Val Ser Glu Leu Arg His Gln Leu Gln
 835 840 845

TCT CGG CAG CAG CTC CGC TCC CGG CGC CAC CCA CCG ACA CCC CCA GAA 2592
 Ser Arg Gln Gln Leu Arg Ser Arg Arg His Pro Pro Thr Pro Pro Glu
 850 855 860

25 CCC TCT GGG GGC CTG CCC AGG GGA CCC CCT GAG CCC CCC GAC CGG CTT 2640
 Pro Ser Gly Gly Leu Pro Arg Gly Pro Pro Glu Pro Pro Asp Arg Leu
 865 870 875 880

30 AGC TGT GAT GGG AGT CGA GTG CAT TTG CTT TAT AAG TGA 2679
 Ser Cys Asp Gly Ser Arg Val His Leu Leu Tyr Lys *
 885 890

35 (2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 892 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly
 1 5 10 15
 5
 Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile
 20 25 30
 Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg
 10 35 40 45
 Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu
 50 55 60
 15 Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys
 65 70 75 80
 Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys
 85 90 95
 20 Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe Pro Met Ser Gly Gly
 100 105 110
 Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val Glu Met Ala Leu Glu
 25 115 120 125
 Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp Tyr Glu Leu Lys Leu
 130 135 140
 30 Ile His His Asp Ser Lys Cys Asp Pro Gly Gln Ala Thr Lys Tyr Leu
 145 150 155 160
 Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile Ile Leu Met Pro Gly
 165 170 175
 35 Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala Ala Arg Met Trp Asn
 180 185 190
 Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro Ala Leu Ser Asn Arg
 40 195 200 205
 Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro Ser Ala Thr Leu His
 210 215 220

Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp Gly Trp Lys Lys Ile
 225 230 235 240

5 Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr Ser Thr Leu Asp Asp
 245 250 255

Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu Ile Thr Phe Arg Gln
 260 265 270

10 Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys Asn Leu Lys Arg Gln
 275 280 285

Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu Thr Glu Ala Arg Lys
 15 290 295 300

Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe Gly Lys Lys Tyr Val
 305 310 315 320

20 Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp Phe Lys Ile Tyr Asp
 325 330 335

Pro Ser Ile Asn Cys Thr Val Asp Glu Met Thr Glu Ala Val Glu Gly
 340 345 350

25 His Ile Thr Thr Glu Ile Val Met Leu Asn Pro Ala Asn Thr Arg Ser
 355 360 365

Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu Lys Leu Thr Lys Arg
 30 370 375 380

Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe Gln Glu Ala Pro Leu
 385 390 395 400

35 Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala Leu Asn Lys Thr Ser
 405 410 415

Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu Asp Phe Asn Tyr Asn
 420 425 430

40 Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala Met Asn Ser Ser Ser
 435 440 445

Phe Glu Gly Val Ser Gly His Val Val Phe Asp Ala Ser Gly Ser Arg
 450 455 460

Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly Gly Ser Tyr Lys Lys
 5 465 470 475 480

Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu Ser Trp Ser Lys Thr
 485 490 495

10 Asp Lys Trp Ile Gly Gly Ser Pro Pro Ala Asp Gln Thr Leu Val Ile
 500 505 510

Lys Thr Phe Arg Phe Leu Ser Gln Lys Leu Phe Ile Ser Val Ser Val
 515 520 525

15 Leu Ser Ser Leu Gly Ile Val Leu Ala Val Val Cys Leu Ser Phe Asn
 530 535 540

Ile Tyr Asn Ser His Val Arg Tyr Ile Gln Asn Ser Gln Pro Asn Leu
 20 545 550 555 560

Asn Asn Leu Thr Ala Val Gly Cys Ser Leu Ala Leu Ala Ala Val Phe
 565 570 575

25 Pro Leu Gly Leu Asp Gly Tyr His Ile Gly Arg Asn Gln Phe Pro Phe
 580 585 590

Val Cys Gln Ala Arg Leu Trp Leu Leu Gly Leu Gly Phe Ser Leu Gly
 595 600 605

30 Tyr Gly Ser Met Phe Thr Lys Ile Trp Trp Val His Thr Val Phe Thr
 610 615 620

Lys Lys Glu Glu Lys Lys Glu Trp Arg Lys Thr Leu Glu Pro Trp Lys
 35 625 630 635 640

Leu Tyr Ala Thr Val Gly Leu Leu Val Gly Met Asp Val Leu Thr Leu
 645 650 655

40 Ala Ile Trp Gln Ile Val Asp Pro Leu His Arg Thr Ile Glu Thr Phe
 660 665 670

Ala Lys Glu Glu Pro Lys Glu Asp Ile Asp Val Ser Ile Leu Pro Gln

	675	680	685
	Leu Glu His Cys Ser Ser Arg Lys Met Asn Thr Trp Leu Gly Ile Phe		
	690	695	700
5	Tyr Gly Tyr Lys Gly Leu Leu Leu Leu Leu Gly Ile Phe Leu Ala Tyr		
	705	710	715 720
	Glu Thr Lys Ser Val Ser Thr Glu Lys Ile Asn Asp His Arg Ala Val		
10		725	730 735
	Gly Met Ala Ile Tyr Asn Val Ala Val Leu Cys Leu Ile Thr Ala Pro		
	740	745	750
15	Val Thr Met Ile Leu Ser Ser Gln Gln Asp Ala Ala Phe Ala Phe Ala		
	755	760	765
	Ser Leu Ala Ile Val Phe Ser Ser Tyr Ile Thr Leu Val Val Leu Phe		
	770	775	780
20	Val Pro Lys Met Arg Arg Leu Ile Thr Arg Gly Glu Trp Gln Ser Glu		
	785	790	795 800
	Ala Gln Asp Thr Met Lys Thr Gly Ser Ser Thr Asn Asn Asn Glu Glu		
25		805	810 815
	Glu Lys Ser Arg Leu Leu Glu Lys Glu Asn Arg Glu Leu Glu Lys Ile		
	820	825	830
30	Ile Ala Glu Lys Glu Glu Arg Val Ser Glu Leu Arg His Gln Leu Gln		
	835	840	845
	Ser Arg Gln Gln Leu Arg Ser Arg Arg His Pro Pro Thr Pro Pro Glu		
	850	855	860
35	Pro Ser Gly Gly Leu Pro Arg Gly Pro Pro Glu Pro Pro Asp Arg Leu		
	865	870	875 880
	Ser Cys Asp Gly Ser Arg Val His Leu Leu Tyr Lys		
40		885	890

(2) INFORMATION FOR SEQ ID NO: 76:

H1865-1 WO SEQ

145

SUBSTITUTE SHEET (RULE 26)

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2661 base pairs

(B) TYPE: nucleic acid

5 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

10 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

15 (A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..2661

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

ATG TTG CTG CTG CTG CTA CTG GCG CCA CTC TTC CTC CGC CCC CCG GGC	48
Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly	
25 1 5 10 15	
GCG GGC GGG GCG CAG ACC CCC AAC GCC ACC TCA GAA GGT TGC CAG ATC	96
Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile	
20 25 30	
30 ATA CAC CCG CCC TGG GAA GGG GGC ATC AGG TAC CGG GGC CTG ACT CGG	144
Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg	
35 40 45	
35 GAC CAG GTG AAG GCT ATC AAC TTC CTG CCA GTG GAC TAT GAG ATT GAG	192
Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu	
50 55 60	
TAT GTG TGC CGG GGG GAG CGC GAG GTG GTG GGG CCC AAG GTC CGC AAG	240
40 Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys	
65 70 75 80	
TGC CTG GCC AAC GGC TCC TGG ACA GAT ATG GAC ACA CCC AGC CGC TGT	288

	Cys	Leu	Ala	Asn	Gly	Ser	Trp	Thr	Asp	Met	Asp	Thr	Pro	Ser	Arg	Cys	
					85					90					95		
	GTG	AAT	CGA	ACG	CCA	CAC	TCA	GAA	CGG	CGC	GCA	GTG	TAC	ATC	GGG	GCA	336
5	Val	Asn	Arg	Thr	Pro	His	Ser	Glu	Arg	Arg	Ala	Val	Tyr	Ile	Gly	Ala	
					100					105					110		
	CTG	TTT	CCC	GCG	GTG	GAG	ATG	GCG	CTG	GAG	GAC	GTG	AAT	AGC	CGC	AGG	384
10	Leu	Phe	Pro	Ala	Val	Glu	Met	Ala	Leu	Glu	Asp	Val	Asn	Ser	Arg	Arg	
					115					120					125		
	GAC	ATC	CTG	CCG	GAC	TAT	GAG	CTC	AAG	CTC	ATC	CAC	CAC	GAC	AGC	AAG	432
	Asp	Ile	Leu	Pro	Asp	Tyr	Glu	Leu	Lys	Leu	Ile	His	His	Asp	Ser	Lys	
					130					135					140		
15	TGT	GAT	CCA	GGC	CAA	GCC	ACC	AAG	TAC	CTA	TAT	GAG	CTG	CTC	TAC	AAC	480
	Cys	Asp	Pro	Gly	Gln	Ala	Thr	Lys	Tyr	Leu	Tyr	Glu	Leu	Leu	Tyr	Asn	
					145					150					155		160
20	GAC	CCT	ATC	AAG	ATC	ATC	CTT	ATG	CCT	GGC	TGC	AGC	TCT	GTC	TCC	ACG	528
	Asp	Pro	Ile	Lys	Ile	Ile	Leu	Met	Pro	Gly	Cys	Ser	Ser	Val	Ser	Thr	
					165					170					175		
	CTG	GTG	GCT	GAG	GCT	GCT	AGG	ATG	TGG	AAC	CTC	ATT	GTG	CTT	TCC	TAT	576
25	Leu	Val	Ala	Glu	Ala	Ala	Arg	Met	Trp	Asn	Leu	Ile	Val	Leu	Ser	Tyr	
					180					185					190		
	GGC	TCC	AGC	TCA	CCA	GCC	CTG	TCA	AAC	CGG	CAG	CGT	TTC	CCC	ACT	TTC	624
30	Gly	Ser	Ser	Ser	Pro	Ala	Leu	Ser	Asn	Arg	Gln	Arg	Phe	Pro	Thr	Phe	
					195					200					205		
	TTC	CGA	ACG	CAC	CCA	TCA	GCC	ACA	CTC	CAC	AAC	CCT	ACC	CGC	GTG	AAA	672
	Phe	Arg	Thr	His	Pro	Ser	Ala	Thr	Leu	His	Asn	Pro	Thr	Arg	Val	Lys	
					210					215					220		
35	CTC	TTT	GAA	AAG	TGG	GGC	TGG	AAG	AAG	ATT	GCT	ACC	ATC	CAG	CAG	ACC	720
	Leu	Phe	Glu	Lys	Trp	Gly	Trp	Lys	Lys	Ile	Ala	Thr	Ile	Gln	Gln	Thr	
					225					230					235		240
40	ACT	GAG	GTC	TTC	ACT	TCG	ACT	CTG	GAC	GAC	CTG	GAG	GAA	CGA	GTG	AAG	768
	Thr	Glu	Val	Phe	Thr	Ser	Thr	Leu	Asp	Asp	Leu	Glu	Glu	Arg	Val	Lys	
					245					250					255		

	GAG GCT GGA ATT GAG ATT ACT TTC CGC CAG AGT TTC TTC TCA GAT CCA	816
	Glu Ala Gly Ile Glu Ile Thr Phe Arg Gln Ser Phe Phe Ser Asp Pro	
	260 265 270	
5	GCT GTG CCC GTC AAA AAC CTG AAG CGC CAG GAT GCC CGA ATC ATC GTG	864
	Ala Val Pro Val Lys Asn Leu Lys Arg Gln Asp Ala Arg Ile Ile Val	
	275 280 285	
	GGA CTT TTC TAT GAG ACT GAA GCC CGG AAA GTT TTT TGT GAG GTG TAC	912
10	Gly Leu Phe Tyr Glu Thr Glu Ala Arg Lys Val Phe Cys Glu Val Tyr	
	290 295 300	
	AAG GAG CGT CTC TTT GGG AAG AAG TAC GTC TGG TTC CTC ATT GGG TGG	960
	Lys Glu Arg Leu Phe Gly Lys Lys Tyr Val Trp Phe Leu Ile Gly Trp	
15	305 310 315 320	
	TAT GCT GAC AAT TGG TTC AAG ATC TAC GAC CCT TCT ATC AAC TGC ACA	1008
	Tyr Ala Asp Asn Trp Phe Lys Ile Tyr Asp Pro Ser Ile Asn Cys Thr	
	325 330 335	
20	GTG GAT GAG ATG ACT GAG GCG GTG GAG GGC CAC ATC ACA ACT GAG ATT	1056
	Val Asp Glu Met Thr Glu Ala Val Glu Gly His Ile Thr Thr Glu Ile	
	340 345 350	
25	GTC ATG CTG AAT CCT GCC AAT ACC CGC AGC ATT TCC AAC ATG ACA TCC	1104
	Val Met Leu Asn Pro Ala Asn Thr Arg Ser Ile Ser Asn Met Thr Ser	
	355 360 365	
	CAG GAA TTT GTG GAG AAA CTA ACC AAG CGA CTG AAA AGA CAC CCT GAG	1152
30	Gln Glu Phe Val Glu Lys Leu Thr Lys Arg Leu Lys Arg His Pro Glu	
	370 375 380	
	GAG ACA GGA GGC TTC CAG GAG GCA CCG CTG GCC TAT GAT GCC ATC TGG	1200
	Glu Thr Gly Gly Phe Gln Glu Ala Pro Leu Ala Tyr Asp Ala Ile Trp	
35	385 390 395 400	
	GCC TTG GCA CTG GCC CTG AAC AAG ACA TCT GGA GGA GGC GGC CGT TCT	1248
	Ala Leu Ala Leu Ala Leu Asn Lys Thr Ser Gly Gly Gly Gly Arg Ser	
	405 410 415	
40	GGT GTG CGC CTG GAG GAC TTC AAC TAC AAC AAC CAG ACC ATT ACC GAC	1296
	Gly Val Arg Leu Glu Asp Phe Asn Tyr Asn Asn Gln Thr Ile Thr Asp	
	420 425 430	

	CAA ATC TAC CGG GCA ATG AAC TCT TCG TCC TTT GAG GGT GTC TCT GGC	1344
	Gln Ile Tyr Arg Ala Met Asn Ser Ser Ser Phe Glu Gly Val Ser Gly	
	435 440 445	
5	CAT GTG GTG TTT GAT GCC AGC GGC TCT CGG ATG GCA TGG ACG CTT ATC	1392
	His Val Val Phe Asp Ala Ser Gly Ser Arg Met Ala Trp Thr Leu Ile	
	450 455 460	
10	GAG CAG CTT CAG GGT GGC AGC TAC AAG AAG ATT GGC TAC TAT GAC AGC	1440
	Glu Gln Leu Gln Gly Gly Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser	
	465 470 475 480	
15	ACC AAG GAT GAT CTT TCC TGG TCC AAA ACA GAT AAA TGG ATT GGA GGG	1488
	Thr Lys Asp Asp Leu Ser Trp Ser Lys Thr Asp Lys Trp Ile Gly Gly	
	485 490 495	
20	TCC CCC CCA GCT GAC CAG ACC CTG GTC ATC AAG ACA TTC CGC TTC CTG	1536
	Ser Pro Pro Ala Asp Gln Thr Leu Val Ile Lys Thr Phe Arg Phe Leu	
	500 505 510	
25	TCA CAG AAA CTC TTT ATC TCC GTC TCA GTT CTC TCC AGC CTG GGC ATT	1584
	Ser Gln Lys Leu Phe Ile Ser Val Ser Val Leu Ser Ser Leu Gly Ile	
	515 520 525	
30	GTC CTA GCT GTT GTC TGT CTG TCC TTT AAC ATC TAC AAC TCA CAT GTC	1632
	Val Leu Ala Val Val Cys Leu Ser Phe Asn Ile Tyr Asn Ser His Val	
	530 535 540	
35	CGT TAT ATC CAG AAC TCA CAG CCC AAC CTG AAC AAC CTG ACT GCT GTG	1680
	Arg Tyr Ile Gln Asn Ser Gln Pro Asn Leu Asn Asn Leu Thr Ala Val	
	545 550 555 560	
40	GGC TGC TCA CTG GCT TTA GCT GCT GTC TTC CCC CTG GGG CTC GAT GGT	1728
	Gly Cys Ser Leu Ala Leu Ala Ala Val Phe Pro Leu Gly Leu Asp Gly	
	565 570 575	
45	TAC CAC ATT GGG AGG AAC CAG TTT CCT TTC GTC TGC CAG GCC CGC CTC	1776
	Tyr His Ile Gly Arg Asn Gln Phe Pro Phe Val Cys Gln Ala Arg Leu	
	580 585 590	
50	TGG CTC CTG GGC CTG GGC TTT AGT CTG GGC TAC GGT TCC ATG TTC ACC	1824
	Trp Leu Leu Gly Leu Gly Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr	

	595	600	605	
	AAG ATT TGG TGG GTC CAC ACG GTC TTC ACA AAG AAG GAA GAA AAG AAG			1872
	Lys Ile Trp Trp Val His Thr Val Phe Thr Lys Lys Glu Glu Lys Lys			
5	610	615	620	
	GAG TGG AGG AAG ACT CTG GAA CCC TGG AAG CTG TAT GCC ACA GTG GGC			1920
	Glu Trp Arg Lys Thr Leu Glu Pro Trp Lys Leu Tyr Ala Thr Val Gly			
	625	630	635	640
10	CTG CTG GTG GGC ATG GAT GTC CTC ACT CTC GCC ATC TGG CAG ATC GTG			1968
	Leu Leu Val Gly Met Asp Val Leu Thr Leu Ala Ile Trp Gln Ile Val			
	645	650	655	
15	GAC CCT CTG CAC CGG ACC ATT GAG ACA TTT GCC AAG GAG GAA CCT AAG			2016
	Asp Pro Leu His Arg Thr Ile Glu Thr Phe Ala Lys Glu Glu Pro Lys			
	660	665	670	
	GAA GAT ATT GAC GTC TCT ATT CTG CCC CAG CTG GAG CAT TGC AGC TCC			2064
20	Glu Asp Ile Asp Val Ser Ile Leu Pro Gln Leu Glu His Cys Ser Ser			
	675	680	685	
	AGG AAG ATG AAT ACA TGG CTT GGC ATT TTC TAT GGT TAC AAG GGG CTG			2112
	Arg Lys Met Asn Thr Trp Leu Gly Ile Phe Tyr Gly Tyr Lys Gly Leu			
25	690	695	700	
	CTG CTG CTG CTG GGA ATC TTC CTT GCT TAT GAG ACC AAG AGT GTG TCC			2160
	Leu Leu Leu Leu Gly Ile Phe Leu Ala Tyr Glu Thr Lys Ser Val Ser			
	705	710	715	720
30	ACT GAG AAG ATC AAT GAT CAC CGG GCT GTG GGC ATG GCT ATC TAC AAT			2208
	Thr Glu Lys Ile Asn Asp His Arg Ala Val Gly Met Ala Ile Tyr Asn			
	725	730	735	
35	GTG GCA GTC CTG TGC CTC ATC ACT GCT CCT GTC ACC ATG ATT CTG TCG			2256
	Val Ala Val Leu Cys Leu Ile Thr Ala Pro Val Thr Met Ile Leu Ser			
	740	745	750	
	AGC CAG CAG GAT GCA GCC TTT GCC TTT GCC TCT CTT GCC ATA GTT TTC			2304
40	Ser Gln Gln Asp Ala Ala Phe Ala Phe Ala Ser Leu Ala Ile Val Phe			
	755	760	765	
	TCC TCC TAT ATC ACT CTT GTT GTG CTC TTT GTG CCC AAG ATG CGC AGG			2352

	Ser	Ser	Tyr	Ile	Thr	Leu	Val	Val	Leu	Phe	Val	Pro	Lys	Met	Arg	Arg	
	770						775					780					
	CTG	ATC	ACC	CGA	GGG	GAA	TGG	CAG	TCG	GAG	GCG	CAG	GAC	ACC	ATG	AAG	2400
5	Leu	Ile	Thr	Arg	Gly	Glu	Trp	Gln	Ser	Glu	Ala	Gln	Asp	Thr	Met	Lys	
	785					790				795					800		
	ACA	GGG	TCA	TCG	ACC	AAC	AAC	AAC	GAG	GAG	GAG	AAG	TCC	CGG	CTG	TTG	2448
	Thr	Gly	Ser	Ser	Thr	Asn	Asn	Asn	Glu	Glu	Glu	Lys	Ser	Arg	Leu	Leu	
10					805				810						815		
	GAG	AAG	GAG	AAC	CGT	GAA	CTG	GAA	AAG	ATC	ATT	GCT	GAG	AAA	GAG	GAG	2496
	Glu	Lys	Glu	Asn	Arg	Glu	Leu	Glu	Lys	Ile	Ile	Ala	Glu	Lys	Glu	Glu	
				820				825					830				
15	CGT	GTC	TCT	GAA	CTG	CGC	CAT	CAA	CTC	CAG	TCT	CGG	CAG	CAG	CTC	CGC	2544
	Arg	Val	Ser	Glu	Leu	Arg	His	Gln	Leu	Gln	Ser	Arg	Gln	Gln	Leu	Arg	
				835				840					845				
20	TCC	CGG	CGC	CAC	CCA	CCG	ACA	CCC	CCA	GAA	CCC	TCT	GGG	GGC	CTG	CCC	2592
	Ser	Arg	Arg	His	Pro	Pro	Thr	Pro	Pro	Glu	Pro	Ser	Gly	Gly	Leu	Pro	
		850					855					860					
	AGG	GGA	CCC	CCT	GAG	CCC	CCC	GAC	CGG	CTT	AGC	TGT	GAT	GGG	AGT	CGA	2640
25	Arg	Gly	Pro	Pro	Glu	Pro	Pro	Asp	Arg	Leu	Ser	Cys	Asp	Gly	Ser	Arg	
	865				870					875				880			
	GTG	CAT	TTG	CTT	TAT	AAG	TGA										2661
	Val	His	Leu	Leu	Tyr	Lys	*										
30					885												

(2) INFORMATION FOR SEQ ID NO: 77:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 886 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly
 1 5 10 15

Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile
 5 20 25 30

Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg
 35 40 45

10 Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu
 50 55 60

Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys
 65 70 75 80

15 Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys
 85 90 95

Val Asn Arg Thr Pro His Ser Glu Arg Arg Ala Val Tyr Ile Gly Ala
 20 100 105 110

Leu Phe Pro Ala Val Glu Met Ala Leu Glu Asp Val Asn Ser Arg Arg
 115 120 125

25 Asp Ile Leu Pro Asp Tyr Glu Leu Lys Leu Ile His His Asp Ser Lys
 130 135 140

Cys Asp Pro Gly Gln Ala Thr Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn
 145 150 155 160

30 Asp Pro Ile Lys Ile Ile Leu Met Pro Gly Cys Ser Ser Val Ser Thr
 165 170 175

Leu Val Ala Glu Ala Ala Arg Met Trp Asn Leu Ile Val Leu Ser Tyr
 35 180 185 190

Gly Ser Ser Ser Pro Ala Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe
 195 200 205

40 Phe Arg Thr His Pro Ser Ala Thr Leu His Asn Pro Thr Arg Val Lys
 210 215 220

Leu Phe Glu Lys Trp Gly Trp Lys Lys Ile Ala Thr Ile Gln Gln Thr

225 230 235 240
 Thr Glu Val Phe Thr Ser Thr Leu Asp Asp Leu Glu Glu Arg Val Lys
 245 250 255
 5
 Glu Ala Gly Ile Glu Ile Thr Phe Arg Gln Ser Phe Phe Ser Asp Pro
 260 265 270
 Ala Val Pro Val Lys Asn Leu Lys Arg Gln Asp Ala Arg Ile Ile Val
 10 275 280 285
 Gly Leu Phe Tyr Glu Thr Glu Ala Arg Lys Val Phe Cys Glu Val Tyr
 290 295 300
 15 Lys Glu Arg Leu Phe Gly Lys Lys Tyr Val Trp Phe Leu Ile Gly Trp
 305 310 315 320
 Tyr Ala Asp Asn Trp Phe Lys Ile Tyr Asp Pro Ser Ile Asn Cys Thr
 325 330 335
 20 Val Asp Glu Met Thr Glu Ala Val Glu Gly His Ile Thr Thr Glu Ile
 340 345 350
 Val Met Leu Asn Pro Ala Asn Thr Arg Ser Ile Ser Asn Met Thr Ser
 25 355 360 365
 Gln Glu Phe Val Glu Lys Leu Thr Lys Arg Leu Lys Arg His Pro Glu
 370 375 380
 30 Glu Thr Gly Gly Phe Gln Glu Ala Pro Leu Ala Tyr Asp Ala Ile Trp
 385 390 395 400
 Ala Leu Ala Leu Ala Leu Asn Lys Thr Ser Gly Gly Gly Gly Arg Ser
 405 410 415
 35 Gly Val Arg Leu Glu Asp Phe Asn Tyr Asn Asn Gln Thr Ile Thr Asp
 420 425 430
 Gln Ile Tyr Arg Ala Met Asn Ser Ser Ser Phe Glu Gly Val Ser Gly
 40 435 440 445
 His Val Val Phe Asp Ala Ser Gly Ser Arg Met Ala Trp Thr Leu Ile
 450 455 460

Glu Gln Leu Gln Gly Gly Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser
 465 470 475 480

5 Thr Lys Asp Asp Leu Ser Trp Ser Lys Thr Asp Lys Trp Ile Gly Gly
 485 490 495

Ser Pro Pro Ala Asp Gln Thr Leu Val Ile Lys Thr Phe Arg Phe Leu
 500 505 510

10 Ser Gln Lys Leu Phe Ile Ser Val Ser Val Leu Ser Ser Leu Gly Ile
 515 520 525

Val Leu Ala Val Val Cys Leu Ser Phe Asn Ile Tyr Asn Ser His Val
 15 530 535 540

Arg Tyr Ile Gln Asn Ser Gln Pro Asn Leu Asn Asn Leu Thr Ala Val
 545 550 555 560

20 Gly Cys Ser Leu Ala Leu Ala Ala Val Phe Pro Leu Gly Leu Asp Gly
 565 570 575

Tyr His Ile Gly Arg Asn Gln Phe Pro Phe Val Cys Gln Ala Arg Leu
 580 585 590

25 Trp Leu Leu Gly Leu Gly Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr
 595 600 605

Lys Ile Trp Trp Val His Thr Val Phe Thr Lys Lys Glu Glu Lys Lys
 30 610 615 620

Glu Trp Arg Lys Thr Leu Glu Pro Trp Lys Leu Tyr Ala Thr Val Gly
 625 630 635 640

35 Leu Leu Val Gly Met Asp Val Leu Thr Leu Ala Ile Trp Gln Ile Val
 645 650 655

Asp Pro Leu His Arg Thr Ile Glu Thr Phe Ala Lys Glu Glu Pro Lys
 660 665 670

40 Glu Asp Ile Asp Val Ser Ile Leu Pro Gln Leu Glu His Cys Ser Ser
 675 680 685

Arg Lys Met Asn Thr Trp Leu Gly Ile Phe Tyr Gly Tyr Lys Gly Leu
 690 695 700

Leu Leu Leu Leu Gly Ile Phe Leu Ala Tyr Glu Thr Lys Ser Val Ser
 5 705 710 715 720

Thr Glu Lys Ile Asn Asp His Arg Ala Val Gly Met Ala Ile Tyr Asn
 725 730 735

10 Val Ala Val Leu Cys Leu Ile Thr Ala Pro Val Thr Met Ile Leu Ser
 740 745 750

Ser Gln Gln Asp Ala Ala Phe Ala Phe Ala Ser Leu Ala Ile Val Phe
 755 760 765

15 Ser Ser Tyr Ile Thr Leu Val Val Leu Phe Val Pro Lys Met Arg Arg
 770 775 780

Leu Ile Thr Arg Gly Glu Trp Gln Ser Glu Ala Gln Asp Thr Met Lys
 20 785 790 795 800

Thr Gly Ser Ser Thr Asn Asn Asn Glu Glu Glu Lys Ser Arg Leu Leu
 805 810 815

25 Glu Lys Glu Asn Arg Glu Leu Glu Lys Ile Ile Ala Glu Lys Glu Glu
 820 825 830

Arg Val Ser Glu Leu Arg His Gln Leu Gln Ser Arg Gln Gln Leu Arg
 835 840 845

30 Ser Arg Arg His Pro Pro Thr Pro Pro Glu Pro Ser Gly Gly Leu Pro
 850 855 860

Arg Gly Pro Pro Glu Pro Pro Asp Arg Leu Ser Cys Asp Gly Ser Arg
 35 865 870 875 880

Val His Leu Leu Tyr Lys
 885

40

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1692 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

10

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS

15

(B) LOCATION:1..1692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

20	ATG TTG CTG CTG CTG CTA CTG GCG CCA CTC TTC CTC CGC CCC CCG GGC	48
	Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly	
	1 5 10 15	
25	GCG GGC GGG GCG CAG ACC CCC AAC GCC ACC TCA GAA GGT TGC CAG ATC	96
	Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile	
	20 25 30	
30	ATA CAC CCG CCC TGG GAA GGG GGC ATC AGG TAC CGG GGC CTG ACT CGG	144
	Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg	
	35 40 45	
35	GAC CAG GTG AAG GCT ATC AAC TTC CTG CCA GTG GAC TAT GAG ATT GAG	192
	Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu	
	50 55 60	
40	TAT GTG TGC CGG GGG GAG CGC GAG GTG GTG GGG CCC AAG GTC CGC AAG	240
	Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys	
	65 70 75 80	
	TGC CTG GCC AAC GGC TCC TGG ACA GAT ATG GAC ACA CCC AGC CGC TGT	288
	Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys	
	85 90 95	
	GTC CGA ATC TGC TCC AAG TCT TAT TTG ACC ATT ACC GAC CAA ATC TAC	336

	Val	Arg	Ile	Cys	Ser	Lys	Ser	Tyr	Leu	Thr	Ile	Thr	Asp	Gln	Ile	Tyr	
				100					105					110			
	CGG	GCA	ATG	AAC	TCT	TCG	TCC	TTT	GAG	GGT	GTC	TCT	GGC	CAT	GTG	GTG	384
5	Arg	Ala	Met	Asn	Ser	Ser	Ser	Phe	Glu	Gly	Val	Ser	Gly	His	Val	Val	
				115				120					125				
	TTT	GAT	GCC	AGC	GGC	TCT	CGG	ATG	GCA	TGG	ACG	CTT	ATC	GAG	CAG	CTT	432
10	Phe	Asp	Ala	Ser	Gly	Ser	Arg	Met	Ala	Trp	Thr	Leu	Ile	Glu	Gln	Leu	
				130				135					140				
	CAG	GGT	GGC	AGC	TAC	AAG	AAG	ATT	GGC	TAC	TAT	GAC	AGC	ACC	AAG	GAT	480
	Gln	Gly	Gly	Ser	Tyr	Lys	Lys	Ile	Gly	Tyr	Tyr	Asp	Ser	Thr	Lys	Asp	
	145					150					155				160		
15	GAT	CTT	TCC	TGG	TCC	AAA	ACA	GAT	AAA	TGG	ATT	GGA	GGG	TCC	CCC	CCA	528
	Asp	Leu	Ser	Trp	Ser	Lys	Thr	Asp	Lys	Trp	Ile	Gly	Gly	Ser	Pro	Pro	
						165				170					175		
20	GCT	GAC	CAG	ACC	CTG	GTC	ATC	AAG	ACA	TTC	CGC	TTC	CTG	TCA	CAG	AAA	576
	Ala	Asp	Gln	Thr	Leu	Val	Ile	Lys	Thr	Phe	Arg	Phe	Leu	Ser	Gln	Lys	
						180				185					190		
	CTC	TTT	ATC	TCC	GTC	TCA	GTT	CTC	TCC	AGC	CTG	GGC	ATT	GTC	CTA	GCT	624
25	Leu	Phe	Ile	Ser	Val	Ser	Val	Leu	Ser	Ser	Leu	Gly	Ile	Val	Leu	Ala	
						195				200					205		
	GTT	GTC	TGT	CTG	TCC	TTT	AAC	ATC	TAC	AAC	TCA	CAT	GTC	CGT	TAT	ATC	672
	Val	Val	Cys	Leu	Ser	Phe	Asn	Ile	Tyr	Asn	Ser	His	Val	Arg	Tyr	Ile	
30						210				215					220		
	CAG	AAC	TCA	CAG	CCC	AAC	CTG	AAC	AAC	CTG	ACT	GCT	GTG	GGC	TGC	TCA	720
	Gln	Asn	Ser	Gln	Pro	Asn	Leu	Asn	Asn	Leu	Thr	Ala	Val	Gly	Cys	Ser	
	225					230				235					240		
35	CTG	GCT	TTA	GCT	GCT	GTC	TTC	CCC	CTG	GGG	CTC	GAT	GGT	TAC	CAC	ATT	768
	Leu	Ala	Leu	Ala	Ala	Val	Phe	Pro	Leu	Gly	Leu	Asp	Gly	Tyr	His	Ile	
						245				250					255		
40	GGG	AGG	AAC	CAG	TTT	CCT	TTC	GTC	TGC	CAG	GCC	CGC	CTC	TGG	CTC	CTG	816
	Gly	Arg	Asn	Gln	Phe	Pro	Phe	Val	Cys	Gln	Ala	Arg	Leu	Trp	Leu	Leu	
						260				265					270		

	GGC	CTG	GGC	TTT	AGT	CTG	GGC	TAC	GGT	TCC	ATG	TTC	ACC	AAG	ATT	TGG	864
	Gly	Leu	Gly	Phe	Ser	Leu	Gly	Tyr	Gly	Ser	Met	Phe	Thr	Lys	Ile	Trp	
			275					280					285				
5	TGG	GTC	CAC	ACG	GTC	TTC	ACA	AAG	AAG	GAA	GAA	AAG	AAG	GAG	TGG	AGG	912
	Trp	Val	His	Thr	Val	Phe	Thr	Lys	Lys	Glu	Glu	Lys	Lys	Glu	Trp	Arg	
			290					295					300				
	AAG	ACT	CTG	GAA	CCC	TGG	AAG	CTG	TAT	GCC	ACA	GTG	GGC	CTG	CTG	GTG	960
10	Lys	Thr	Leu	Glu	Pro	Trp	Lys	Leu	Tyr	Ala	Thr	Val	Gly	Leu	Leu	Val	
			305					310					315			320	
	GGC	ATG	GAT	GTC	CTC	ACT	CTC	GCC	ATC	TGG	CAG	ATC	GTG	GAC	CCT	CTG	1008
	Gly	Met	Asp	Val	Leu	Thr	Leu	Ala	Ile	Trp	Gln	Ile	Val	Asp	Pro	Leu	
15					325					330					335		
	CAC	CGG	ACC	ATT	GAG	ACA	TTT	GCC	AAG	GAG	GAA	CCT	AAG	GAA	GAT	ATT	1056
	His	Arg	Thr	Ile	Glu	Thr	Phe	Ala	Lys	Glu	Glu	Pro	Lys	Glu	Asp	Ile	
				340						345					350		
20	GAC	GTC	TCT	ATT	CTG	CCC	CAG	CTG	GAG	CAT	TGC	AGC	TCC	AGG	AAG	ATG	1104
	Asp	Val	Ser	Ile	Leu	Pro	Gln	Leu	Glu	His	Cys	Ser	Ser	Arg	Lys	Met	
				355				360						365			
25	AAT	ACA	TGG	CTT	GGC	ATT	TTC	TAT	GGT	TAC	AAG	GGG	CTG	CTG	CTG	CTG	1152
	Asn	Thr	Trp	Leu	Gly	Ile	Phe	Tyr	Gly	Tyr	Lys	Gly	Leu	Leu	Leu	Leu	
			370					375					380				
	CTG	GGA	ATC	TTC	CTT	GCT	TAT	GAG	ACC	AAG	AGT	GTG	TCC	ACT	GAG	AAG	1200
30	Leu	Gly	Ile	Phe	Leu	Ala	Tyr	Glu	Thr	Lys	Ser	Val	Ser	Thr	Glu	Lys	
			385					390				395				400	
	ATC	AAT	GAT	CAC	CGG	GCT	GTG	GGC	ATG	GCT	ATC	TAC	AAT	GTG	GCA	GTC	1248
	Ile	Asn	Asp	His	Arg	Ala	Val	Gly	Met	Ala	Ile	Tyr	Asn	Val	Ala	Val	
35					405					410					415		
	CTG	TGC	CTC	ATC	ACT	GCT	CCT	GTC	ACC	ATG	ATT	CTG	TCC	AGC	CAG	CAG	1296
	Leu	Cys	Leu	Ile	Thr	Ala	Pro	Val	Thr	Met	Ile	Leu	Ser	Ser	Gln	Gln	
				420						425					430		
40	GAT	GCA	GCC	TTT	GCC	TTT	GCC	TCT	CTT	GCC	ATA	GTT	TTC	TCC	TCC	TAT	1344
	Asp	Ala	Ala	Phe	Ala	Phe	Ala	Ser	Leu	Ala	Ile	Val	Phe	Ser	Ser	Tyr	
				435						440					445		

ATC ACT CTT GTT GTG CTC TTT GTG CCC AAG ATG CGC AGG CTG ATC ACC 1392
 Ile Thr Leu Val Val Leu Phe Val Pro Lys Met Arg Arg Leu Ile Thr
 450 455 460

5 CGA GGG GAA TGG CAG TCG GAG GCG CAG GAC ACC ATG AAG ACA GGG TCA 1440
 Arg Gly Glu Trp Gln Ser Glu Ala Gln Asp Thr Met Lys Thr Gly Ser
 465 470 475 480

10 TCG ACC AAC AAC AAC GAG GAG GAG AAG TCC CGG CTG TTG GAG AAG GAG 1488
 Ser Thr Asn Asn Asn Glu Glu Glu Lys Ser Arg Leu Leu Glu Lys Glu
 485 490 495

AAC CGT GAA CTG GAA AAG ATC ATT GCT GAG AAA GAG GAG CGT GTC TCT 1536
 15 Asn Arg Glu Leu Glu Lys Ile Ile Ala Glu Lys Glu Glu Arg Val Ser
 500 505 510

GAA CTG CGC CAT CAA CTC CAG TCT CGG CAG CAG CTC CGC TCC CGG CGC 1584
 Glu Leu Arg His Gln Leu Gln Ser Arg Gln Gln Leu Arg Ser Arg Arg
 20 515 520 525

CAC CCA CCG ACA CCC CCA GAA CCC TCT GGG GGC CTG CCC AGG GGA CCC 1632
 His Pro Pro Thr Pro Pro Glu Pro Ser Gly Gly Leu Pro Arg Gly Pro
 530 535 540

25 CCT GAG CCC CCC GAC CGG CTT AGC TGT GAT GGG AGT CGA GTG CAT TTG 1680
 Pro Glu Pro Pro Asp Arg Leu Ser Cys Asp Gly Ser Arg Val His Leu
 545 550 555 560

30 CTT TAT AAG TGA 1692
 Leu Tyr Lys *

35 (2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 563 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly
 1 5 10 15
 5
 Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile
 20 25 30
 Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg
 10 35 40 45
 Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu
 50 55 60
 15 Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys
 65 70 75 80
 Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys
 85 90 95
 20 Val Arg Ile Cys Ser Lys Ser Tyr Leu Thr Ile Thr Asp Gln Ile Tyr
 100 105 110
 Arg Ala Met Asn Ser Ser Ser Phe Glu Gly Val Ser Gly His Val Val
 25 115 120 125
 Phe Asp Ala Ser Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln Leu
 130 135 140
 30 Gln Gly Gly Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys Asp
 145 150 155 160
 Asp Leu Ser Trp Ser Lys Thr Asp Lys Trp Ile Gly Gly Ser Pro Pro
 165 170 175
 35 Ala Asp Gln Thr Leu Val Ile Lys Thr Phe Arg Phe Leu Ser Gln Lys
 180 185 190
 Leu Phe Ile Ser Val Ser Val Leu Ser Ser Leu Gly Ile Val Leu Ala
 40 195 200 205
 Val Val Cys Leu Ser Phe Asn Ile Tyr Asn Ser His Val Arg Tyr Ile
 210 215 220

Gln Asn Ser Gln Pro Asn Leu Asn Asn Leu Thr Ala Val Gly Cys Ser
 225 230 235 240

5 Leu Ala Leu Ala Ala Val Phe Pro Leu Gly Leu Asp Gly Tyr His Ile
 245 250 255

Gly Arg Asn Gln Phe Pro Phe Val Cys Gln Ala Arg Leu Trp Leu Leu
 260 265 270

10 Gly Leu Gly Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr Lys Ile Trp
 275 280 285

Trp Val His Thr Val Phe Thr Lys Lys Glu Glu Lys Lys Glu Trp Arg
 15 290 295 300

Lys Thr Leu Glu Pro Trp Lys Leu Tyr Ala Thr Val Gly Leu Leu Val
 305 310 315 320

20 Gly Met Asp Val Leu Thr Leu Ala Ile Trp Gln Ile Val Asp Pro Leu
 325 330 335

His Arg Thr Ile Glu Thr Phe Ala Lys Glu Glu Pro Lys Glu Asp Ile
 340 345 350

25 Asp Val Ser Ile Leu Pro Gln Leu Glu His Cys Ser Ser Arg Lys Met
 355 360 365

Asn Thr Trp Leu Gly Ile Phe Tyr Gly Tyr Lys Gly Leu Leu Leu Leu
 30 370 375 380

Leu Gly Ile Phe Leu Ala Tyr Glu Thr Lys Ser Val Ser Thr Glu Lys
 385 390 395 400

35 Ile Asn Asp His Arg Ala Val Gly Met Ala Ile Tyr Asn Val Ala Val
 405 410 415

Leu Cys Leu Ile Thr Ala Pro Val Thr Met Ile Leu Ser Ser Gln Gln
 420 425 430

40 Asp Ala Ala Phe Ala Phe Ala Ser Leu Ala Ile Val Phe Ser Ser Tyr
 435 440 445

Ile Thr Leu Val Val Leu Phe Val Pro Lys Met Arg Arg Leu Ile Thr
450 455 460

Arg Gly Glu Trp Gln Ser Glu Ala Gln Asp Thr Met Lys Thr Gly Ser
5 465 470 475 480

Ser Thr Asn Asn Asn Glu Glu Glu Lys Ser Arg Leu Leu Glu Lys Glu
485 490 495

10 Asn Arg Glu Leu Glu Lys Ile Ile Ala Glu Lys Glu Glu Arg Val Ser
500 505 510

Glu Leu Arg His Gln Leu Gln Ser Arg Gln Gln Leu Arg Ser Arg Arg
515 520 525

15 His Pro Pro Thr Pro Pro Glu Pro Ser Gly Gly Leu Pro Arg Gly Pro
530 535 540

Pro Glu Pro Pro Asp Arg Leu Ser Cys Asp Gly Ser Arg Val His Leu
20 545 550 555 560

Leu Tyr Lys

25

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 2602 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

40

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

	ATG TTG CTG CTG CTG CTA CTG GCG CCA CTC TTC CTC CGC CCC CCG GGC	48
5	Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly	
	1 5 10 15	
	GCG GGC GGG GCG CAG ACC CCC AAC GCC ACC TCA GAA GGT TGC CAG ATC	96
	Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile	
10	20 25 30	
	ATA CAC CCG CCC TGG GAA GGG GGC ATC AGG TAC CGG GGC CTG ACT CGG	144
	Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg	
	35 40 45	
15	GAC CAG GTG AAG GCT ATC AAC TTC CTG CCA GTG GAC TAT GAG ATT GAT	192
	Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Asp	
	50 55 60	
20	GAA TCG AAC GCC ACA CTC AGA ACG GCG CGC AGT GTA CAT CGG GGC ACT	240
	Glu Ser Asn Ala Thr Leu Arg Thr Ala Arg Ser Val His Arg Gly Thr	
	65 70 75 80	
	GTT TCC CAT GAG CGG GGG CTG GCC AGG GGG CCA GGC CTG CCA GCC CGC	288
25	Val Ser His Glu Arg Gly Leu Ala Arg Gly Pro Gly Leu Pro Ala Arg	
	85 90 95	
	GGT GGA GAT GGC GCT GGA GGA CGT GAA TAG CCGCAGGGAC ATCCTGCCGG	338
	Gly Gly Asp Gly Ala Gly Gly Arg Glu *	
30	100 105	
	ACTATGAGCT CAAGCTCATC CACCACGACA GCAAGTGTGA TCCAGGCCAA GCCACCAAGT	398
	ACCTATATGA GCTGCTCTAC AACGACCCTA TCAAGATCAT CCTTATGCCT GGCTGCAGCT	458
35	CTGTCTCCAC GCTGGTGGCT GAGGCTGCTA GGATGTGGAA CCTCATTGTG CTTTCCTATG	518
	GCTCCAGCTC ACCAGCCCTG TCAAACCGGC AGCGTTTCCC CACTTTCTTC CGAACGCACC	578
40	CATCAGCCAC ACTCCACAAC CCTACCCGCG TGAACTCTT TGAAAAGTGG GGCTGGAAGA	638
	AGATTGCTAC CATCCAGCAG ACCACTGAGG TCTTCACTTC GACTCTGGAC GACCTGGAGG	698

	AACGAGTGAA GGAGGCTGGA ATTGAGATTA CTTTCCGCCA GAGTTTCTTC TCAGATCCAG	758
	CTGTGCCCCGT CAAAAACCTG AAGCGCCAGG ATGCCCGAAT CATCGTGGGA CTTTTCTATG	818
5	AGACTGAAGC CCGGAAAGTT TTTTGTGAGG TGTACAAGGA GCGTCTCTTT GGAAGAAGT	878
	ACGTCTGGTT CCTCATTGGG TGGTATGCTG ACAATTGGTT CAAGATCTAC GACCCTTCTA	938
	TCAACTGCAC AGTGGATGAG ATGACTGAGG CGGTGGAGGG CCACATCACA ACTGAGATTG	998
10	TCATGCTGAA TCCTGCCAAT ACCCGCAGCA TTTCCAACAT GACATCCCAG GAATTTGTGG	1058
	AGAAACTAAC CAAGCGACTG AAAAGACACC CTGAGGAGAC AGGAGGCTTC CAGGAGGCAC	1118
15	CGCTGGCCTA TGATGCCATC TGGGCCTTGG CACTGGCCCT GAACAAGACA TCTGGAGGAG	1178
	GCGGCCGTTC TGGTGTGCGC CTGGAGGACT TCAACTACAA CAACCAGACC ATTACCGACC	1238
	AAATCTACCG GGCAATGAAC TCTTCGTCTT TTAGGGTGT CTCTGGCCAT GTGGTGTGTTG	1298
20	ATGCCAGCGG CTCTCGGATG GCATGGACGC TTATCGAGCA GCTTCAGGGT GGCAGCTACA	1358
	AGAAGATTGG CTACTATGAC AGCACCAAGG ATGATCTTTC CTGGTCCAAA ACAGATAAAT	1418
25	GGATTGGAGG GTCCCCCCA GCTGACCAGA CCCTGGTCAT CAAGACATTC CGCTTCCTGT	1478
	CACAGAACT CTTTATCTCC GTCTCAGTTC TCTCCAGCCT GGGCATTGTC CTAGCTGTTG	1538
	TCTGTCTGTC CTTTAACATC TACAACTCAC ATGTCCGTTA TATCCAGAAC TCACAGCCCA	1598
30	ACCTGAACAA CCTGACTGCT GTGGGCTGCT CACTGGCTTT AGCTGCTGTC TTCCCCCTGG	1658
	GGCTCGATGG TTACCACATT GGGAGGAACC AGTTTCCTTT CGTCTGCCAG GCCCGCCTCT	1718
35	GGCTCCTGGG CCTGGGCTTT AGTCTGGGCT ACGGTTCCAT GTTACCAAG ATTTGGTGGG	1778
	TCCACACGGT CTTCAAAAAG AAGGAAGAAA AGAAGGAGTG GAGGAAGACT CTGGAACCCT	1838
	GGAAGCTGTA TGCCACAGTG GGCCTGCTGG TGGCATGGA TGTCTCACT CTCGCCATCT	1898
40	GGCAGATCGT GGACCCTCTG CACCGGACCA TTGAGACATT TGCCAAGGAG GAACCTAAGG	1958
	AAGATATTGA CGTCTCTATT CTGCCCCAGC TGGAGCATTG CAGCTCCAGG AAGATGAATA	2018

CATGGCTTGG CATTTTCTAT GGTTACAAGG GGCTGCTGCT GCTGCTGGGA ATCTTCCTTG 2078
 CTTATGAGAC CAAGAGTGTG TCCACTGAGA AGATCAATGA TCACCGGGCT GTGGGCATGG 2138
 5 CTATCTACAA TGTGGCAGTC CTGTGCCTCA TCACTGCTCC TGTCACCATG ATTCTGTCCA 2198
 GCCAGCAGGA TGCAGCCTTT GCCTTTGCCT CTCTTGCCAT AGTTTTCTCC TCCTATATCA 2258
 10 CTCTTGTGTG GCTCTTTGTG CCCAAGATGC GCAGGCTGAT CACCCGAGGG GAATGGCAGT 2318
 CGGAGGCGCA GGACACCATG AAGACAGGGT CATCGACCAA CAACAACGAG GAGGAGAAGT 2378
 CCCGGCTGTT GGAGAAGGAG AACCGTGAAC TGGAAAAGAT CATTGCTGAG AAAGAGGAGC 2438
 15 GTGTCTCTGA ACTGCGCCAT CAACTCCAGT CTCGGCAGCA GCTCCGCTCC CGGCGCCACC 2498
 CACCGACACC CCCAGAACCC TCTGGGGGCC TGCCCAGGGG ACCCCCTGAG CCCCCGACC 2558
 20 GGCTTAGCTG TGATGGGAGT CGAGTGCATT TGCTTTATAA GTGA 2602

(2) INFORMATION FOR SEQ ID NO: 81:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly
 35 1 5 10 15
 Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile
 20 25 30
 40 Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg
 35 40 45
 Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Asp

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      50              55              60
Glu Ser Asn Ala Thr Leu Arg Thr Ala Arg Ser Val His Arg Gly Thr
 65              70              75              80
5
Val Ser His Glu Arg Gly Leu Ala Arg Gly Pro Gly Leu Pro Ala Arg
      85              90              95
Gly Gly Asp Gly Ala Gly Gly Arg Glu
10              100              105

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(2) INFORMATION FOR SEQ ID NO: 82:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2367 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

25 (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

	ATG	TTG	CTG	CTG	CTG	CTA	CTG	GCG	CCA	CTC	TTC	CTC	CGC	CCC	CCG	GGC	48
35	Met	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Pro	Leu	Phe	Leu	Arg	Pro	Pro	Gly	
	1					5				10					15		
	GCG	GGC	GGG	GCG	CAG	ACC	CCC	AAC	GCC	ACC	TCA	GAA	GGT	TGC	CAG	ATC	96
	Ala	Gly	Gly	Ala	Gln	Thr	Pro	Asn	Ala	Thr	Ser	Glu	Gly	Cys	Gln	Ile	
40					20				25					30			
	ATA	CAC	CCG	CCC	TGG	GAA	GGG	GGC	ATC	AGG	TAC	CGG	GGC	CTG	ACT	CGG	144
	Ile	His	Pro	Pro	Trp	Glu	Gly	Gly	Ile	Arg	Tyr	Arg	Gly	Leu	Thr	Arg	

	35	40	45	
	GAC CAG GTG AAG GCT ATC AAC TTC CTG CCA GTG GAC TAT GAG ATT GAG			192
	Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu			
5	50	55	60	
	TAT GTG TGC CGG GGG GAG CGC GAG GTG GTG GGG CCC AAG GTC CGC AAG			240
	Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys			
	65	70	75	80
10				
	TGC CTG GCC AAC GGC TCC TGG ACA GAT ATG GAC ACA CCC AGC CGC TGT			288
	Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys			
	85	90	95	
15	GTG TGA TCCAGGCCAA GCCACCAAGT ACCTATATGA GCTGCTCTAC AACGACCCTA			344
	Val *			
	TCAAGATCAT CCTTATGCCT GGCTGCAGCT CTGTCTCCAC GCTGGTGGCT GAGGCTGCTA			404
20				
	GGATGTGGAA CCTCATTGTG CTTTCCTATG GCTCCAGCTC ACCAGCCCTG TCAAACCGGC			464
	AGCGTTTCCC CACTTTCTTC CGAACGCACC CATCAGCCAC ACTCCACAAC CCTACCCGCG			524
25	TGAAACTCTT TGAAAAGTGG GGCTGGAAGA AGATTGCTAC CATCCAGCAG ACCACTGAGG			584
	TCTTCACTTC GACTCTGGAC GACCTGGAGG AACGAGTGAA GGAGGCTGGA ATTGAGATTA			644
	CTTTCCGCCA GAGTTTCTTC TCAGATCCAG CTGTGCCCCGT CAAAACCTG AAGCGCCAGG			704
30	ATGCCCCGAAT CATCGTGCGA CTTTCTATG AGACTGAAGC CCGGAAAGTT TTTTGTGAGG			764
	TGTACAAGGA GCGTCTCTTT GGGAAGAAGT ACGTCTGGTT CCTCATTGGG TGGTATGCTG			824
35	ACAATTGGTT CAAGATCTAC GACCCTTCTA TCAACTGCAC AGTGGATGAG ATGACTGAGG			884
	CGGTGGAGGG CCACATCACA ACTGAGATTG TCATGCTGAA TCCTGCCAAT ACCCGCAGCA			944
	TTTCCAACAT GACATCCCAG GAATTTGTGG AGAACTAAC CAAGCGACTG AAAAGACACC			1004
40	CTGAGGAGAC AGGAGGCTTC CAGGAGGCAC CGCTGGCCTA TGATGCCATC TGGGCCTTGG			1064
	CACTGGCCCT GAACAAGACA TCTGGAGGAG GCGGCCGTTC TGGTGTGCGC CTGGAGGACT			1124

	TCAACTACAA	CAACCAGACC	ATTACCGACC	AAATCTACCG	GGCAATGAAC	TCTTCGTCCT	1184
	TTGAGGGTGT	CTCTGGCCAT	GTGGTGTTTG	ATGCCAGCGG	CTCTCGGATG	GCATGGACGC	1244
5	TTATCGAGCA	GCTTCAGGGT	GGCAGCTACA	AGAAGATTGG	CTACTATGAC	AGCACCAAGG	1304
	ATGATCTTTC	CTGGTCCAAA	ACAGATAAAT	GGATTGTTAT	ATCCAGAACT	CACAGCCCAA	1364
10	CCTGAACAAC	CTGACTGCTG	TGGGCTGCTC	ACTGGCTTTA	GCTGCTGTCT	TCCCCCTGGG	1424
	GCTCGATGGT	TACCACATTG	GGAGGAACCA	GTTTCCTTTC	GTCTGCCAGG	CCCGCCTCTG	1484
	GCTCCTGGGC	CTGGGCTTTA	GTCTGGGCTA	CGGTTCCATG	TTCACCAAGA	TTTGGTGGGT	1544
15	CCACACGGTC	TTCACAAAGA	AGGAAGAAAA	GAAGGAGTGG	AGGAAGACTC	TGGAACCCTG	1604
	GAAGCTGTAT	GCCACAGTGG	GCCTGCTGGT	GGGCATGGAT	GTCCCTCACTC	TCGCCATCTG	1664
20	GCAGATCGTG	GACCCTCTGC	ACCGGACCAT	TGAGACATTT	GCCAAGGAGG	AACCTAAGGA	1724
	AGATATTGAC	GTCTCTATTC	TGCCCCAGCT	GGAGCATTGC	AGCTCCAGGA	AGATGAATAC	1784
	ATGGCTTGGC	ATTTTCTATG	GTTACAAGGG	GCTGCTGCTG	CTGCTGGGAA	TCTTCCTTGC	1844
25	TTATGAGACC	AAGAGTGTGT	CCACTGAGAA	GATCAATGAT	CACCGGGCTG	TGGGCATGGC	1904
	TATCTACAAT	GTGGCAGTCC	TGTGCCTCAT	CACTGCTCCT	GTCACCATGA	TTCTGTCCAG	1964
30	CCAGCAGGAT	GCAGCCTTTG	CCTTTGCCTC	TCTTGCCATA	GTTTTCTCCT	CCTATATCAC	2024
	TCTTGTTGTG	CTCTTTGTGC	CCAAGATGCG	CAGGCTGATC	ACCCGAGGGG	AATGGCAGTC	2084
	GGAGGCGCAG	GACACCATGA	AGACAGGGTC	ATCGACCAAC	AACAACGAGG	AGGAGAAGTC	2144
35	CCGGCTGTTG	GAGAAGGAGA	ACCGTGAACT	GGAAAAGATC	ATTGCTGAGA	AAGAGGAGCG	2204
	TGTCTCTGAA	CTGCGCCATC	AACTCCAGTC	TCGGCAGCAG	CTCCGCTCCC	GGCGCCACCC	2264
40	ACCGACACCC	CCAGAACCCT	CTGGGGGCCT	GCCCAGGGGA	CCCCCTGAGC	CCCCCGACCG	2324
	GCTTAGCTGT	GATGGGAGTC	GAGTGCATTT	GCTTTATAAG	TGA		2367

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 97 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly
1 5 10 15
Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile
20 25 30
Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg
20 35 40 45
Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu
50 55 60
Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys
25 65 70 75 80
Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys
85 90 95
30 Val

35 (2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 2489 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

10

(A) NAME/KEY: CDS

(B) LOCATION:1..1491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

15	ATG TTG CTG CTG CTG CTA CTG GCG CCA CTC TTC CTC CGC CCC CCG GGC	48
	Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly	
	1 5 10 15	
	GCG GGC GGG GCG CAG ACC CCC AAC GCC ACC TCA GAA GGT TGC CAG ATC	96
20	Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile	
	20 25 30	
	ATA CAC CCG CCC TGG GAA GGG GGC ATC AGG TAC CGG GGC CTG ACT CGG	144
	Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg	
25	35 40 45	
	GAC CAG GTG AAG GCT ATC AAC TTC CTG CCA GTG GAC TAT GAG ATT GAG	192
	Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu	
	50 55 60	
30	TAT GTG TGC CGG GGG GAG CGC GAG GTG GTG GGG CCC AAG GTC CGC AAG	240
	Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys	
	65 70 75 80	
35	TGC CTG GCC AAC GGC TCC TGG ACA GAT ATG GAC ACA CCC AGC CGC TGT	288
	Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys	
	85 90 95	
	GTC CGA ATC TGC TCC AAG TCT TAT TTG ACC CTG GAA AAT GGG AAG GTT	336
40	Val Arg Ile Cys Ser Lys Ser Tyr Leu Thr Leu Glu Asn Gly Lys Val	
	100 105 110	
	TTC CTG ACG GGT GGG GAC CTC CCA GCT CTG GAC GGA GCC CGG GTG GAT	384

	Phe	Leu	Thr	Gly	Gly	Asp	Leu	Pro	Ala	Leu	Asp	Gly	Ala	Arg	Val	Asp			
	115						120						125						
	TTC	CGG	TGT	GAC	CCC	GAC	TTC	CAT	CTG	TGT	GAT	CCA	GGC	CAA	GCC	ACC	432		
5	Phe	Arg	Cys	Asp	Pro	Asp	Phe	His	Leu	Cys	Asp	Pro	Gly	Gln	Ala	Thr			
	130						135						140						
	AAG	TAC	CTA	TAT	GAG	CTG	CTC	TAC	AAC	GAC	CCT	ATC	AAG	ATC	ATC	CTT	480		
	Lys	Tyr	Leu	Tyr	Glu	Leu	Leu	Tyr	Asn	Asp	Pro	Ile	Lys	Ile	Ile	Leu			
10	145	150						155						160					
	ATG	CCT	GGC	TGC	AGC	TCT	GTC	TCC	ACG	CTG	GTG	GCT	GAG	GCT	GCT	AGG	528		
	Met	Pro	Gly	Cys	Ser	Ser	Val	Ser	Thr	Leu	Val	Ala	Glu	Ala	Ala	Arg			
	165						170						175						
15	ATG	TGG	AAC	CTC	ATT	GTG	CTT	TCC	TAT	GGC	TCC	AGC	TCA	CCA	GCC	CTG	576		
	Met	Trp	Asn	Leu	Ile	Val	Leu	Ser	Tyr	Gly	Ser	Ser	Ser	Pro	Ala	Leu			
	180						185						190						
20	TCA	AAC	CGG	CAG	CGT	TTC	CCC	ACT	TTC	TTC	CGA	ACG	CAC	CCA	TCA	GCC	624		
	Ser	Asn	Arg	Gln	Arg	Phe	Pro	Thr	Phe	Phe	Arg	Thr	His	Pro	Ser	Ala			
	195						200						205						
	ACA	CTC	CAC	AAC	CCT	ACC	CGC	GTG	AAA	CTC	TTT	GAA	AAG	TGG	GGC	TGG	672		
25	Thr	Leu	His	Asn	Pro	Thr	Arg	Val	Lys	Leu	Phe	Glu	Lys	Trp	Gly	Trp			
	210						215						220						
	AAG	AAG	ATT	GCT	ACC	ATC	CAG	CAG	ACC	ACT	GAG	GTC	TTC	ACT	TCG	ACT	720		
	Lys	Lys	Ile	Ala	Thr	Ile	Gln	Gln	Thr	Thr	Glu	Val	Phe	Thr	Ser	Thr			
30	225	230						235						240					
	CTG	GAC	GAC	CTG	GAG	GAA	CGA	GTG	AAG	GAG	GCT	GGA	ATT	GAG	ATT	ACT	768		
	Leu	Asp	Asp	Leu	Glu	Glu	Arg	Val	Lys	Glu	Ala	Gly	Ile	Glu	Ile	Thr			
	245						250						255						
35	TTC	CGC	CAG	AGT	TTC	TTC	TCA	GAT	CCA	GCT	GTG	CCC	GTC	AAA	AAC	CTG	816		
	Phe	Arg	Gln	Ser	Phe	Phe	Ser	Asp	Pro	Ala	Val	Pro	Val	Lys	Asn	Leu			
	260						265						270						
40	AAG	CGC	CAG	GAT	GCC	CGA	ATC	ATC	GTG	GGA	CTT	TTC	TAT	GAG	ACT	GAA	864		
	Lys	Arg	Gln	Asp	Ala	Arg	Ile	Ile	Val	Gly	Leu	Phe	Tyr	Glu	Thr	Glu			
	275						280						285						

	GCC CGG AAA GTT TTT TGT GAG GTG TAC AAG GAG CGT CTC TTT GGG AAG	912
	Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe Gly Lys	
	290 295 300	
5	AAG TAC GTC TGG TTC CTC ATT GGG TGG TAT GCT GAC AAT TGG TTC AAG	960
	Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp Phe Lys	
	305 310 315 320	
	ATC TAC GAC CCT TCT ATC AAC TGC ACA GTG GAT GAG ATG ACT GAG GCG	1008
10	Ile Tyr Asp Pro Ser Ile Asn Cys Thr Val Asp Glu Met Thr Glu Ala	
	325 330 335	
	GTG GAG GGC CAC ATC ACA ACT GAG ATT GTC ATG CTG AAT CCT GCC AAT	1056
	Val Glu Gly His Ile Thr Thr Glu Ile Val Met Leu Asn Pro Ala Asn	
15	340 345 350	
	ACC CGC AGC ATT TCC AAC ATG ACA TCC CAG GAA TTT GTG GAG AAA CTA	1104
	Thr Arg Ser Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu Lys Leu	
	355 360 365	
20	ACC AAG CGA CTG AAA AGA CAC CCT GAG GAG ACA GGA GGC TTC CAG GAG	1152
	Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe Gln Glu	
	370 375 380	
25	GCA CCG CTG GCC TAT GAT GCC ATC TGG GCC TTG GCA CTG GCC CTG AAC	1200
	Ala Pro Leu Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala Leu Asn	
	385 390 395 400	
	AAG ACA TCT GGA GGA GGC GGC CGT TCT GGT GTG CGC CTG GAG GAC TTC	1248
30	Lys Thr Ser Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu Asp Phe	
	405 410 415	
	AAC TAC AAC AAC CAG ACC ATT ACC GAC CAA ATC TAC CGG GCA ATG AAC	1296
	Asn Tyr Asn Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala Met Asn	
35	420 425 430	
	TCT TCG TCC TTT GAG GGT GTC TCT GGC CAT GTG GTG TTT GAT GCC AGC	1344
	Ser Ser Ser Phe Glu Gly Val Ser Gly His Val Val Phe Asp Ala Ser	
	435 440 445	
40	GGC TCT CGG ATG GCA TGG ACG CTT ATC GAG CAG CTT CAG GGT GGC AGC	1392
	Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly Gly Ser	
	450 455 460	

TAC AAG AAG ATT GGC TAC TAT GAC AGC ACC AAG GAT GAT CTT TCC TGG 1440
Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu Ser Trp
465 470 475 480

5 TCC AAA ACA GAT AAA TGG ATT GTT ATA TCC AGA ACT CAC AGC CCA ACC 1488
Ser Lys Thr Asp Lys Trp Ile Val Ile Ser Arg Thr His Ser Pro Thr
485 490 495

10 TGA ACAACCTGAC TGCTGTGGGC TGCTCACTGG CTTTAGCTGC TGTCTTCCCC 1541
*

CTGGGGCTCG ATGGTTACCA CATTGGGAGG AACCAGTTTC CTTTCGTCTG CCAGGCCCGC 1601

15 CTCTGGCTCC TGGGCCTGGG CTTTAGTCTG GGCTACGGTT CCATGTTTAC CAAGATTG 1661

TGGGTCCACA CGGTCTTCAC AAAGAAGGAA GAAAAGAAGG AGTGGAGGAA GACTCTGGAA 1721

20 CCCTGGAAGC TGTATGCCAC AGTGGGCCTG CTGGTGGGCA TGGATGTCCT CACTCTCGCC 1781

ATCTGGCAGA TCGTGGACCC TCTGCACCGG ACCATTGAGA CATTTGCCAA GGAGGAACCT 1841

AAGGAAGATA TTGACGTCTC TATTCTGCCC CAGCTGGAGC ATTGCAGCTC CAGGAAGATG 1901

25 AATACATGGC TTGGCATTTC CTATGGTTAC AAGGGGCTGC TGCTGCTGCT GGGAATCTTC 1961

CTTGCTTATG AGACCAAGAG TGTGTCCACT GAGAAGATCA ATGATCACCG GGCTGTGGGC 2021

30 ATGGCTATCT ACAATGTGGC AGTCCTGTGC CTCATCACTG CTCCTGTCAC CATGATTCTG 2081

TCCAGCCAGC AGGATGCAGC CTTTGCCTTT GCCTCTCTTG CCATAGTTTT CTCCTCCTAT 2141

ATCACTCTTG TTGTGCTCTT TGTGCCCAAG ATGCGCAGGC TGATCACCCG AGGGGAATGG 2201

35 CAGTCGGAGG CGCAGGACAC CATGAAGACA GGGTCATCGA CCAACAACAA CGAGGAGGAG 2261

AAGTCCCGGC TGTTGGAGAA GGAGAACCGT GAACTGGAAA AGATCATTGC TGAGAAAGAG 2321

40 GAGCGTGTCT CTGAACTGCG CCATCAACTC CAGTCTCGGC AGCAGCTCCG CTCCCGGCGC 2381

CACCCACCGA CACCCCCAGA ACCCTCTGGG GGCCTGCCCA GGGGACCCCC TGAGCCCCC 2441

GACCGGCTTA GCTGTGATGG GAGTCGAGTG CATTTGCTTT ATAAGTGA

2489

(2) INFORMATION FOR SEQ ID NO: 85:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 496 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

15 Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly
1 5 10 15

Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile
20 25 30

20 Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg
35 40 45

Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu
25 50 55 60

Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys
65 70 75 80

30 Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys
85 90 95

Val Arg Ile Cys Ser Lys Ser Tyr Leu Thr Leu Glu Asn Gly Lys Val
100 105 110

35 Phe Leu Thr Gly Gly Asp Leu Pro Ala Leu Asp Gly Ala Arg Val Asp
115 120 125

Phe Arg Cys Asp Pro Asp Phe His Leu Cys Asp Pro Gly Gln Ala Thr
40 130 135 140

Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile Ile Leu
145 150 155 160

Met Pro Gly Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala Ala Arg
165 170 175

5 Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro Ala Leu
180 185 190

Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro Ser Ala
195 200 205

10 Thr Leu His Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp Gly Trp
210 215 220

Lys Lys Ile Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr Ser Thr
15 225 230 235 240

Leu Asp Asp Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu Ile Thr
245 250 255

20 Phe Arg Gln Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys Asn Leu
260 265 270

Lys Arg Gln Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu Thr Glu
275 280 285

25 Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe Gly Lys
290 295 300

Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp Phe Lys
30 305 310 315 320

Ile Tyr Asp Pro Ser Ile Asn Cys Thr Val Asp Glu Met Thr Glu Ala
325 330 335

35 Val Glu Gly His Ile Thr Thr Glu Ile Val Met Leu Asn Pro Ala Asn
340 345 350

Thr Arg Ser Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu Lys Leu
355 360 365

40 Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe Gln Glu
370 375 380

Ala Pro Leu Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala Leu Asn
385 390 395 400

Lys Thr Ser Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu Asp Phe
5 405 410 415

Asn Tyr Asn Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala Met Asn
420 425 430

10 Ser Ser Ser Phe Glu Gly Val Ser Gly His Val Val Phe Asp Ala Ser
435 440 445

Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly Gly Ser
450 455 460

15 Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu Ser Trp
465 470 475 480

Ser Lys Thr Asp Lys Trp Ile Val Ile Ser Arg Thr His Ser Pro Thr
20 485 490 495

2

INTERNATIONAL SEARCH REPORT

International application No.

PCT/SE 98/01947

A. CLASSIFICATION OF SUBJECT MATTER

IPC6: C07K 14/705

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC6: C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

SE,DK,FI,NO classes as above

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	EMBL Databas Genbank/DDBJ, accession no. Y11044, Grifa A. et al: "GABA (gamma-amino-butyric acid)neurotransmission: identification and fine mapping of human GABA-B receptor gene"; Biochem. Biophys. Res. Commun. 250:240-245(1998) --	1-6,11-13, 16-26
X	Nature, Volume 386, March 1997, Klemens Kaupmann et al, "Expression cloning of GABAB receptors uncovers similarity to metabotropic glutamate receptors" page 239 - page 246 --	1-6,11-13, 16-26
X	WO 9746675 A1 (NOVARTIS AG), 11 December 1997 (11.12.97), page 50 - page 56, claim 4 --	1-6,11-13, 16-26

☒ Further documents are listed in the continuation of Box C.☒ See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance: the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance: the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search

23 March 1999

Date of mailing of the international search report

26-03-1999

Name and mailing address of the ISA

Swedish Patent Office

Box 5055, S-102 42 STOCKHOLM

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Authorized officer

Patrick Andersson

Telephone No. +46 8 782 25 00

INTERNATIONAL SEARCH REPORT

International application No.

PCT/SE 98/01947

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	Dialog Information Services, File 34, SciSearch, Dialog accession no. 07157158, Goei VL et al: "Human gamma-aminobutyric acid B receptor gene: Complementary DNA cloning, expression, chromosomal location, and genomic organization", Biological Psychiatry, 1998, V44, N8(OCT 15), p659-666 --	1-6,11-13, 16-26
A	Brain Research Bulletin, Volume 38, No 6, 1995, Robert J. Washabau et al, "GABA Receptros in the Dorsal Motor Nucleus of the Vagus Influence Feline Lower Esophageal Sphincter and Gastric Function" page 587 - page 594 -- -----	1-6,11-13, 16-26

INTERNATIONAL SEARCH REPORT

International application No. _____

PCT/SE 98/01947

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

See next page

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐
☐

- The additional search fees were accompanied by the applicant's protest.
No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/SE 98/01947

According to PCT rule 13.2, an international application shall relate to one invention only or a group of inventions linked by one or more of the same or corresponding "special technical features", i.e. features that define a contribution which each of the inventions makes over the prior art.

The claimed invention relates to a nucleic acid sequence encoding a GABAB-receptor from either human or canine origin. A possible special technical features could have been nucleotide sequence encoding a GABAB-receptor. However a nucleotide sequence encoding a human GABAB-receptor is known from Grifa A. et. al., see the search report. Thus, the present application is considered to contain the following independent inventions:

Invention 1, claims 3-4, and the parts of claims 1-2 and 16-26 relating to claims 3-4: A human GABAB-receptor 1a, and related items,

Invention 2, claims 5-6, and the parts of claims 1-2 and 16-26 relating to claims 5-6: A human GABAB-receptor 1b, and related items,

Invention 3, claims 7-8, and the parts of claims 1-2 and 16-26 relating to claims 7-8: A human GABAB-receptor 1c, and related items,

Invention 4, claims 9-10, and the parts of claims 1-2 and 16-26 relating to claims 9-10: A human GABAB-receptor 1d, and related items,

Invention 5, claims 12-13, and the parts of claims 1, 11 and 16-26 relating to claims 12-13: A canine GABAB-receptor 1a, and related items.

Invention 6, claims 14-15, and the parts of claims 1, 11 and 16-26 relating to claims 14-15: A canine GABAB-receptor 1c, and related items.

The search has been limited to inventions 1, 2 and 5.

INTERNATIONAL SEARCH REPORT

Information on patent family members

02/03/99

International application No.

PCT/SE 98/01947

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9746675 A1	11/12/97	AU 2028497 A	05/01/98
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